



GAATTCGGAG GAATTATTCA AAACATAAAC ACAATAAACA ATTTGAGTAG TTGCCGCACA	60
CACACACACA CACAGCCCGT GGATTATTAC ACTAAAAGCG ACACTCAATC CAAAAAATCA	120
GCAACAAAAA CATCAATAAA C ATG CAT TGG ATT AAA TGT TTA TTA ACA GCA	171
Met His Trp Ile Lys Cys Leu Leu Thr Ala	
1 5 10	
TTC ATT TGC TTC ACA GTC ATC GTG CAG GTT CAC AGT TCC GGC AGC TTT	219
Phe Ile Cys Phe Thr Val Ile Val Gln Val His Ser Ser Gly Ser Phe	
15 20 25	
GAG TTG CGC CTG AAG TAC TTC AGC AAC GAT CAC GGG CGG GAC AAC GAG	267
Glu Leu Arg Leu Lys Tyr Phe Ser Asn Asp His Gly Arg Asp Asn Glu	
30 35 40	
GGT CGC TGC TGC AGC GGG GAG TCG GAC GGA GCG ACG GGC AAG TGC CTG	315
Gly Arg Cys Cys Ser Gly Glu Ser Asp Gly Ala Thr Gly Lys Cys Leu	
45 50 55	
GGC AGC TGC AAG ACG CGG TTT CGC GTC TGC CTA AAG CAC TAC CAG GCC	363
Gly Ser Cys Lys Thr Arg Phe Arg Val Cys Leu Lys His Tyr Gln Ala	
60 65 70	
ACC ATC GAC ACC ACC TCC CAG TGC ACC TAC GGG GAC GTG ATC ACG CCC	411
Thr Ile Asp Thr Thr Ser Gln Cys Thr Tyr Gly Asp Val Ile Thr Pro	
75 80 85 90	
ATT CTC GGC GAG AAC TCG GTC AAT CTG ACC GAC GCC CAG CGC TTC CAG	459
Ile Leu Gly Glu Asn Ser Val Asn Leu Thr Asp Ala Gln Arg Phe Gln	
95 100 105	
AAC AAG GGC TTC ACG AAT CCC ATC CAG TTC CCC TTC TCG TTC TCA TGG	507
Asn Lys Gly Phe Thr Asn Pro Ile Gln Phe Pro Phe Ser Phe Ser Trp	
110 115 120	

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FIG.1A

CCG GGT ACC TTC TCG CTG ATC GTC GAG GCC TGG CAT GAT ACG AAC AAT	555
Pro Gly Thr Phe Ser Leu Ile Val Glu Ala Trp His Asp Thr Asn Asn	
125 130 135	
AGC GGC AAT GCG CGA ACC AAC AAG CTC CTC ATC CAG CGA CTC TTG GTG	603
Ser Gly Asn Ala Arg Thr Asn Lys Leu Leu Ile Gln Arg Leu Leu Val	
140 145 150	
CAG CAG GTA CTG GAG GTG TCC TCC GAA TGG AAG ACG AAC AAG TCG GAA	651
Gln Gln Val Leu Glu Val Ser Ser Glu Trp Lys Thr Asn Lys Ser Glu	
155 160 165 170	
TCG CAG TAC ACG TCG CTG GAG TAC GAT TTC CGT GTC ACC TGC GAT CTC	699
Ser Gln Tyr Thr Ser Leu Glu Tyr Asp Phe Arg Val Thr Cys Asp Leu	
175 180 185	
AAC TAC TAC GGA TCC GGC TGT GCC AAG TTC TGC CGG CCC CGC GAC GAT	747
Asn Tyr Tyr Gly Ser Gly Cys Ala Lys Phe Cys Arg Pro Arg Asp Asp	
190 195 200	
TCA TTT GGA CAC TCG ACT TGC TCG GAG ACG GGC GAA ATT ATC TGT TTG	795
Ser Phe Gly His Ser Thr Cys Ser Glu Thr Gly Glu Ile Ile Cys Leu	
205 210 215	
ACC GGA TGG CAG GGC GAT TAC TGT CAC ATA CCC AAA TGC GCC AAA GGC	843
Thr Gly Trp Gln Gly Asp Tyr Cys His Ile Pro Lys Cys Ala Lys Gly	
220 225 230	
TGT GAA CAT GGA CAT TGC GAC AAA CCC AAT CAA TGC GTT TGC CAA CTG	891
Cys Glu His Gly His Cys Asp Lys Pro Asn Gln Cys Val Cys Gln Leu	
235 240 245 250	
GGC TGG AAG GGA GCC TTG TGC AAC GAG TGC GTT CTG GAA CCG AAC TGC	939
Gly Trp Lys Gly Ala Leu Cys Asn Glu Cys Val Leu Glu Pro Asn Cys	
255 260 265	

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FIG.1B

ATC CAT GGC ACC TGC AAC AAA CCC TGG ACT TGC ATC TGC AAC GAG GGT	987
Ile His Gly Thr Cys Asn Lys Pro Trp Thr Cys Ile Cys Asn Glu Gly	
270 275 280	
TGG GGA GGC TTG TAC TGC AAC CAG GAT CTG AAC TAC TGC ACC AAC CAC	1035
Trp Gly Gly Leu Tyr Cys Asn Gln Asp Leu Asn Tyr Cys Thr Asn His	
285 290 295	
AGA CCC TGC AAG AAT GGC GGA ACC TGC TTC AAC ACC GGC GAG GGA TTG	1083
Arg Pro Cys Lys Asn Gly Gly Thr Cys Phe Asn Thr Gly Glu Gly Leu	
300 305 310	
TAC ACA TGC AAA TGC GCT CCA GGA TAC AGT GGT GAT GAT TGC GAA AAT	1131
Tyr Thr Cys Lys Cys Ala Pro Gly Tyr Ser Gly Asp Asp Cys Glu Asn	
315 320 325 330	
GAG ATC TAC TCC TGC GAT GCC GAT GTC AAT CCC TGC CAG AAT GGT GGT	1179
Glu Ile Tyr Ser Cys Asp Ala Asp Val Asn Pro Cys Gln Asn Gly Gly	
335 340 345	
ACC TGC ATC GAT GAG CCG CAC ACA AAA ACC GGC TAC AAG TGT CAT TGC	1227
Thr Cys Ile Asp Glu Pro His Thr Lys Thr Gly Tyr Lys Cys His Cys	
350 355 360	
GCC AAC GGC TGG AGC GGA AAG ATG TGC GAG GAG AAA GTG CTC ACG TGT	1275
Ala Asn Gly Trp Ser Gly Lys Met Cys Glu Glu Lys Val Leu Thr Cys	
365 370 375	
TCG GAC AAA CCC TGT CAT CAG GGA ATC TGC CGC AAC GTT CGT CCT GGC	1323
Ser Asp Lys Pro Cys His Gln Gly Ile Cys Arg Asn Val Arg Pro Gly	
380 385 390	
TTG GGA AGC AAG GGT CAG GGC TAC CAG TGC GAA TGT CCC ATT GGC TAC	1371
Leu Gly Ser Lys Gly Gln Gly Tyr Gln Cys Glu Cys Pro Ile Gly Tyr	
395 400 405 410	

FIG.1C

AGC GGA CCC AAC TGC GAT CTC CAG CTG GAC AAC TGC AGT CCG AAT CCA	1419
Ser Gly Pro Asn Cys Asp Leu Gln Leu Asp Asn Cys Ser Pro Asn Pro	
415 420 425	
TGC ATA AAC GGT GGA AGC TGT CAG CCG AGC GGA AAG TGT ATT TGC CCA	1467
Cys Ile Asn Gly Gly Ser Cys Gln Pro Ser Gly Lys Cys Ile Cys Pro	
430 435 440	
GCG GGA TTT TCG GGA ACG AGA TGC GAG ACC AAC ATT GAC GAT TGT CTT	1515
Ala Gly Phe Ser Gly Thr Arg Cys Glu Thr Asn Ile Asp Asp Cys Leu	
445 450 455	
GGC CAC CAG TGC GAG AAC GGA GGC ACC TGC ATA GAT ATG GTC AAC CAA	1563
Gly His Gln Cys Glu Asn Gly Gly Thr Cys Ile Asp Met Val Asn Gln	
460 465 470	
TAT CGC TGC CAA TGC GTT CCC GGT TTC CAT GGC ACC CAC TGT AGT AGC	1611
Tyr Arg Cys Gln Cys Val Pro Gly Phe His Gly Thr His Cys Ser Ser	
475 480 485 490	
AAA GTT GAC TTG TGC CTC ATC AGA CCG TGT GCC AAT GGA GGA ACC TGC	1659
Lys Val Asp Leu Cys Leu Ile Arg Pro Cys Ala Asn Gly Gly Thr Cys	
495 500 505	
TTG AAT CTC AAC AAC GAT TAC CAG TGC ACC TGT CGT GCG GGA TTT ACT	1707
Leu Asn Leu Asn Asn Asp Tyr Gln Cys Thr Cys Arg Ala Gly Phe Thr	
510 515 520	
GGC AAG GAT TGC TCT GTG GAC ATC GAT GAG TGC AGC AGT GGA CCC TGT	1755
Gly Lys Asp Cys Ser Val Asp Ile Asp Glu Cys Ser Ser Gly Pro Cys	
525 530 535	
CAT AAC GGC GGC ACT TGC ATG AAC CGC GTC AAT TCG TTC GAA TGC GTG	1803
His Asn Gly Gly Thr Cys Met Asn Arg Val Asn Ser Phe Glu Cys Val	
540 545 550	

FIG.1D

TGT GCC AAT GGT TTC AGG GGC AAG CAG TGC GAT GAG GAG TCC TAC GAT	1851
Cys Ala Asn Gly Phe Arg Gly Lys Gln Cys Asp Glu Glu Ser Tyr Asp	
555 560 565 570	
TCG GTG ACC TTC GAT GCC CAC CAA TAT GGA GCG ACC ACA CAA GCG AGA	1899
Ser Val Thr Phe Asp Ala His Gln Tyr Gly Ala Thr Thr Gln Ala Arg	
575 580 585	
GCC GAT GGT TTG ACC AAT GCC CAG GTA GTC CTA ATT GCT GTT TTC TCC	1947
Ala Asp Gly Leu Thr Asn Ala Gln Val Val Leu Ile Ala Val Phe Ser	
590 595 600	
GTT GCG ATG CCT TTG GTG GCG GTT ATT GCG GCG TGC GTG GTC TTC TGC	1995
Val Ala Met Pro Leu Val Ala Val Ile Ala Ala Cys Val Val Phe Cys	
605 610 615	
ATG AAG CGC AAG CGT AAG CGT GCT CAG GAA AAG GAC GAC GCG GAG GCC	2043
Met Lys Arg Lys Arg Lys Arg Ala Gln Glu Lys Asp Asp Ala Glu Ala	
620 625 630	
AGG AAG CAG AAC GAA CAG AAT GCG GTG GCC ACA ATG CAT CAC AAT GGC	2091
Arg Lys Gln Asn Glu Gln Asn Ala Val Ala Thr Met His His Asn Gly	
635 640 645 650	
AGT GGG GTG GGT GTA GCT TTG GCT TCA GCC TCT CTG GGC GGC AAA ACT	2139
Ser Gly Val Gly Val Ala Leu Ala Ser Ala Ser Leu Gly Gly Lys Thr	
655 660 665	
GGC AGC AAC AGC GGT CTC ACC TTC GAT GGC GGC AAC CCG AAT ATC ATC	2187
Gly Ser Asn Ser Gly Leu Thr Phe Asp Gly Gly Asn Pro Asn Ile Ile	
670 675 680	
AAA AAC ACC TGG GAC AAG TCG GTC AAC AAC ATT TGT GCC TCA GCA GCA	2235
Lys Asn Thr Trp Asp Lys Ser Val Asn Asn Ile Cys Ala Ser Ala Ala	
685 690 695	

FIG.1E

GCA GCG GCG GCG GCG GCA GCA GCG GCG GAC GAG TGT CTC ATG TAC GGC Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Asp Glu Cys Leu Met Tyr Gly 700 705 710	2283
GGA TAT GTG GCC TCG GTG GCG GAT AAC AAC AAT GCC AAC TCA GAC TTT Gly Tyr Val Ala Ser Val Ala Asp Asn Asn Asn Ala Asn Ser Asp Phe 715 720 725 730	2331
TGT GTG GCT CCG CTA CAA AGA GCC AAG TCG CAA AAG CAA CTC AAC ACC Cys Val Ala Pro Leu Gln Arg Ala Lys Ser Gln Lys Gln Leu Asn Thr 735 740 745	2379
GAT CCC ACG CTC ATG CAC CGC GGT TCG CCG GCA GGC AGC TCA GCC AAG Asp Pro Thr Leu Met His Arg Gly Ser Pro Ala Gly Ser Ser Ala Lys 750 755 760	2427
GGA GCG TCT GGC GGA GGA CCG GGA GCG GCG GAG GGC AAG AGG ATC TCT Gly Ala Ser Gly Gly Gly Pro Gly Ala Ala Glu Gly Lys Arg Ile Ser 765 770 775	2475
GTT TTA GGC GAG GGT TCC TAC TGT AGC CAG CGT TGG CCC TCG TTG GCG Val Leu Gly Glu Gly Ser Tyr Cys Ser Gln Arg Trp Pro Ser Leu Ala 780 785 790	2523
GCG GCG GGA GTG GCC GGA GCC TGT TCA TCC CAG CTA ATG GCT GCA GCT Ala Ala Gly Val Ala Gly Ala Cys Ser Ser Gln Leu Met Ala Ala Ala 795 800 805 810	2571
TCG GCA GCG GGC AGC GGA GCG GGG ACG GCG CAA CAG CAG CGA TCC GTG Ser Ala Ala Gly Ser Gly Ala Gly Thr Ala Gln Gln Gln Arg Ser Val 815 820 825	2619
GTC TGC GGC ACT CCG CAT ATG TAACTCCAAA AATCCGGAAG GGCTCCTGGT Val Cys Gly Thr Pro His Met 830	2670
AAATCCGGAG AAATCCGCAT GGAGGAGCTG ACAGCACATA CACAAAGAAA AGACTGGGTT	2730
GGGTTCAAAA TGTGAGAGAG ACGCCAAAAT GTTGTGTGTTG ATTGAAGCAG TTTAGTCGTC	2790
ACGAAAAATG AAAAATCTGT AACAGGCATA ACTCGTAAAC TCCCTAAAAA ATTTGTATAG	2850
TAATTAGCAA AGCTGTGACC CAGCCGTTTC GATCCCGAAT TC	2892

FIG.1F

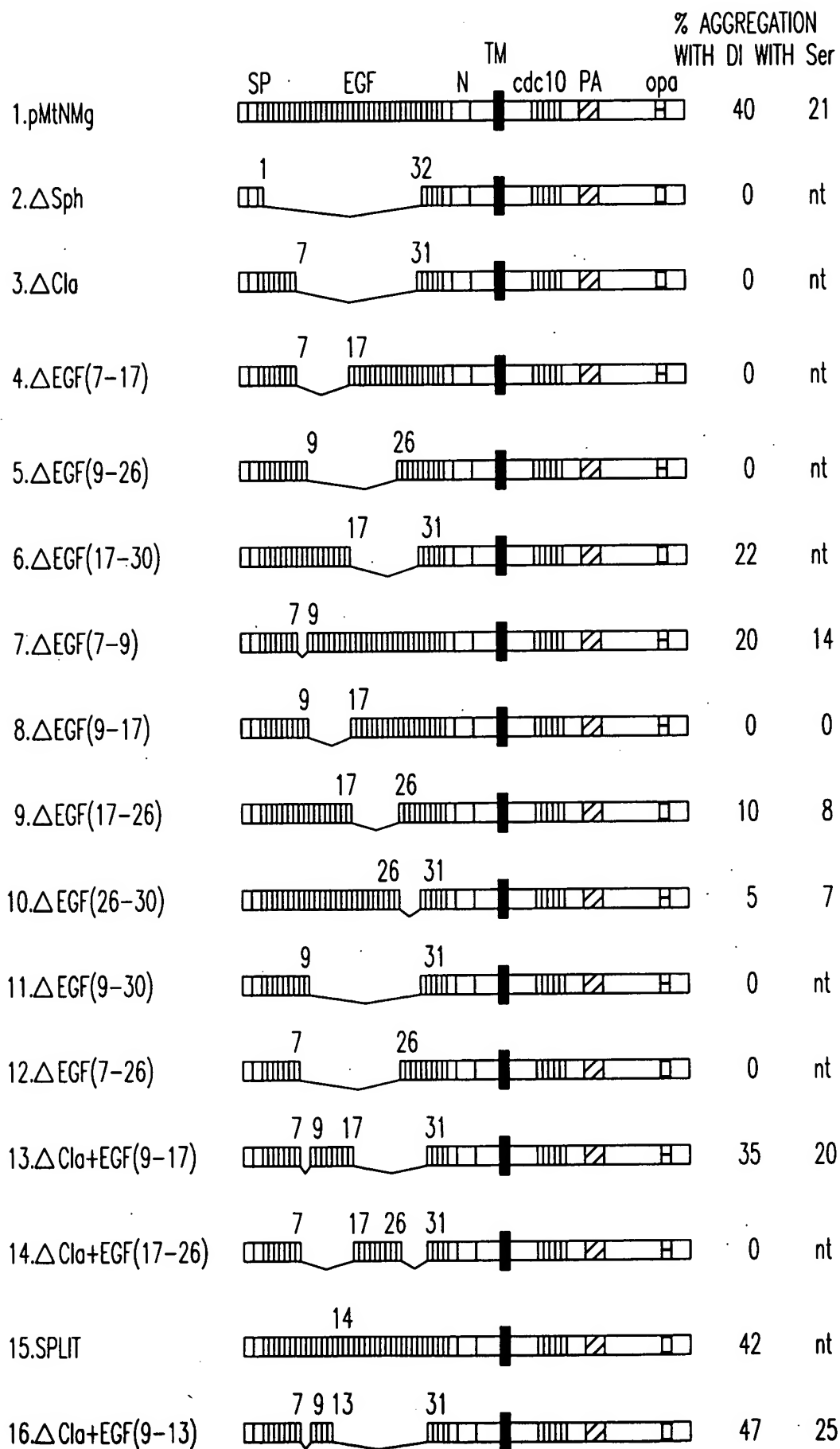


FIG.2A

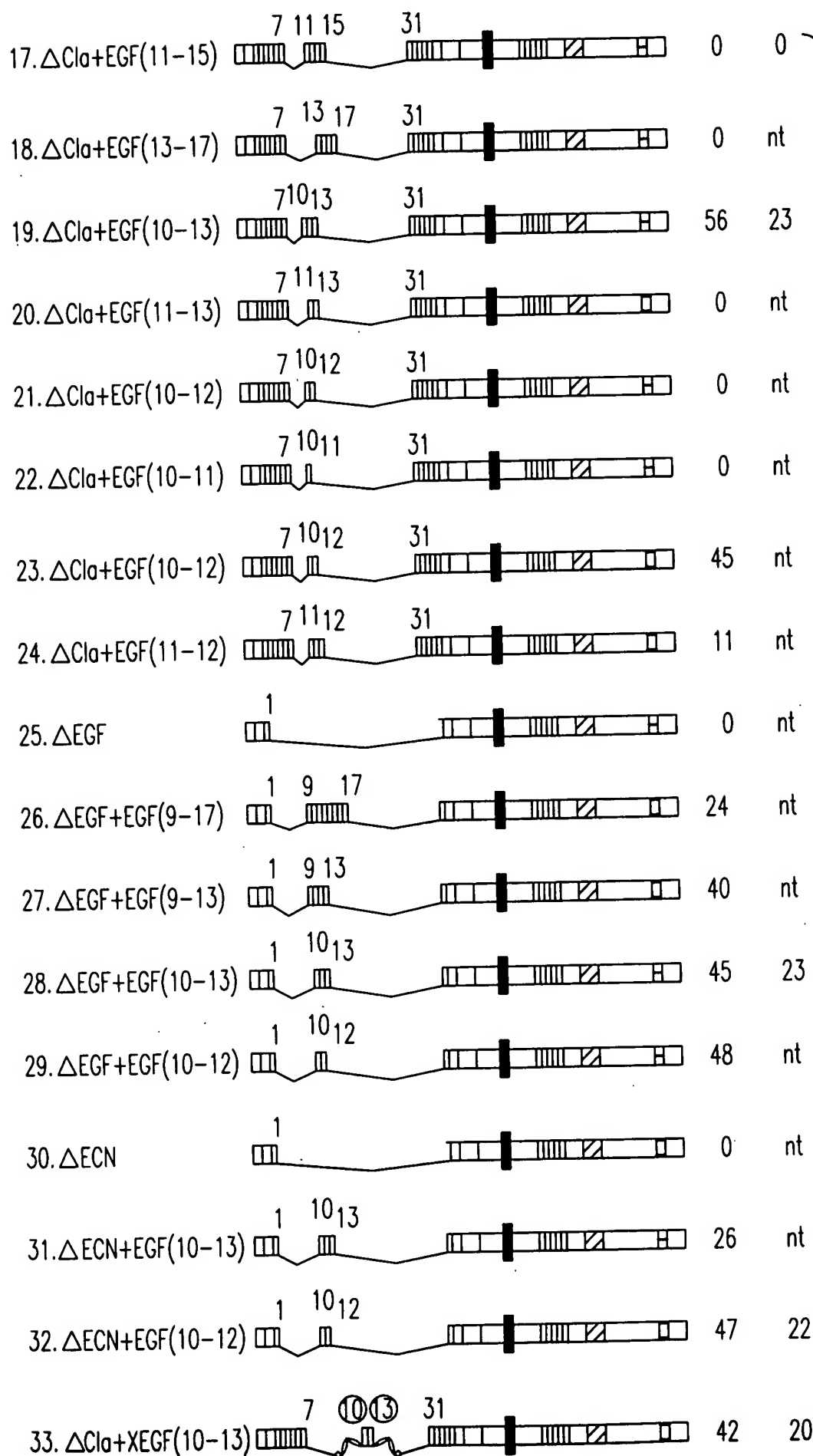
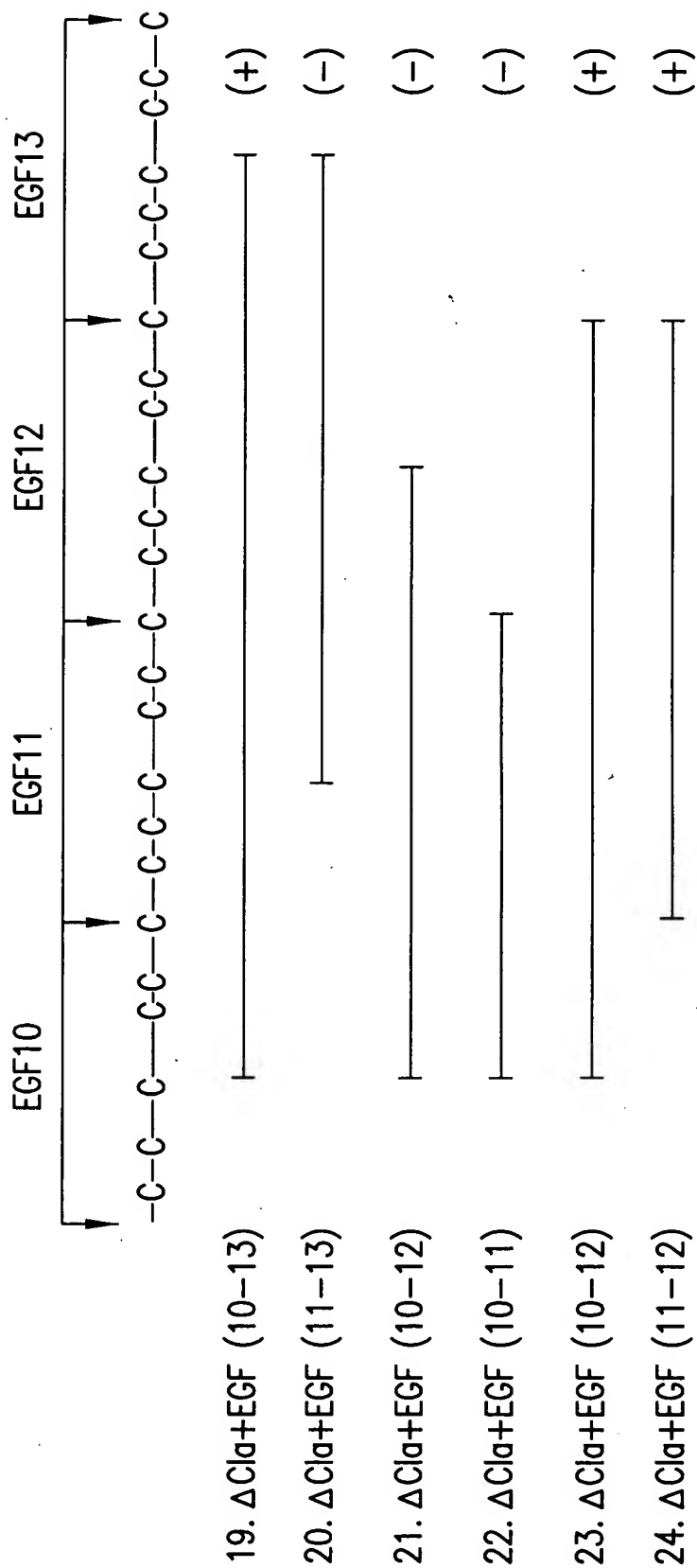


FIG.2B





**FIG. 3**

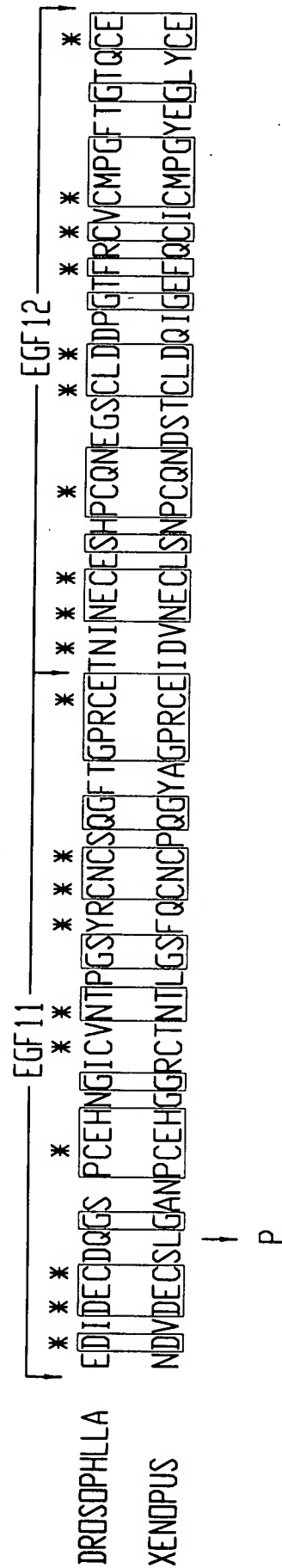


FIG.4

1 CCGAGTCGAGCGCGTGCTTCGAGCGGTGATGAGCCCTTTTCTGTCAACGCTAAAGATC  
121 AAGCACATACTAAGGTCCATATAAATAATAATAATTGTGTGTGATAACAACATTAT  
241 GGGCGTTATTCAGCTATCCAGAGCAAGTGTAGTGTGGCAAAATAGAAACAACAAGGCA  
361 CAATCCAGAGTGAATCCGAAACAACACTCCATCTAGATCGCCCAACCAAGCATCACGCTCGCA  
  
481 TCGTCGTTGGAGTCAACAATAGAAATCAGCAGACAGCCTGGGAATGTCCAAGACGGCG  
SerSerLeuGluSerThrIleGluSerAlaAspSerLeuGlyMetSerLysLysThrAla  
  
601 CGCGATTGTCGATCATTAAAGICTGCCTGCAACTTAATTGCTTTAATTTAATACTGTTA  
ArgAspCysArgSerLeuLysSerAlaCysAsnLeuIleAlaLeuIleLeuIleLeuLeu  
-----  
721 AACAGCCATCTACTCAACGGCTATTGCTGGGCATGCCAGCGGAACCTAGGGCCACCAAG  
AsnSerHisLeuLeuAsnGlyTyrCysCysGlyMetProAlaGluLeuArgAlaThrLys  
  
841 ACQGAGCAGGGTGCCAGCATATCCACGGGCTGTTCGTTTGGCAAGGCCACCAAGATA  
ThrGluGlnGlyAlaSerIleSerThrGlyCysSerPheGlyAsnAlaThrThrLysIle  
#2  
  
961 ACGTTTCGTTGGACGAGTCGTTACGCTGATACTGCAGGCGTTGGATATGTACAACACA  
ThrPheArgTrpThrLysSerPheThrLeuIleLeuGlnAlaLeuAspMetTyrAsnThr  
#3  
1081 TCGCCGGAGTGGAGACGCTGGACCACATCGGGCGGAACGCGGATCACCTACCGTGTC  
SerProGluTrpLysThrLeuAspHisIleGlyArgAsnAlaArgIleThrTyrArgVal  
  
1201 GACGATCAGTTCGGTCACATACGCCCTGGGGCTCCGAGGGTCAGAAAGCTCTGCCTGAATGGC  
AspAspGlnPheGlyHisTyrAlaCysGlySerGluGlyGlnLysLeuCysLeuAsnGly

FIG. 5A

FIG. 5B

TACAAACATCAGCGCCTATCAAGTGAAGTGTCAGTGTGAACAAACAAAACGAGAG  
CCAAACAAAACCAACAAACGAGGCAAGTGGAGAAATGATACAGCATCCAGAGTAC  
CCAAATCTGCATACATGGGCTAATTAGGCTGCCAGCGAATTACATTTGTGGTGC  
AACGCCCCCAGAAATGTACAAAATGTTAGGAACATTTTCGGCGAAACACGCTACGTCG  
MetPheArgLysHisPheArgArgLysProAlaThrSer 13  
ACAAAAGGCAGGTCGGAGGCATCGGTACCCAAAATCGGAGCCCTGCCATCGACGATC  
ThrLysArgGlnArgProArgHisArgValProLysIleAlaThrLeuProSerThrIle 53  
GTCCATAAGATATCCGCAGCTGGTAACCTCGAGCTGGAAATATTAGAAATCTCAAAATACC  
ValHisLysIleSerAlaAlaGlyAsnPheGluLeuGluIleLeuGluIleSerAsnThr 93  
-----#1  
ACGATAGGCTGCTCGCCATGCACGACGGCATTCCTGGCTGTGCCTGAAGGAGTACCAGACC  
ThrIleGlyCysSerProCysThrThrAlaPheArgLeuCysLeuLysGluTyrGlnThr 133  
CTGGGTGGCTCCAGCTTTGTGCTCAGCGATCCGGGTGTGGAGCCATTGTGCTGCCCTTT  
LeuGlyGlySerSerPheValLeuSerAspProGlyValGlyAlaIleValLeuProPhe 173  
TCCTATCCAGATGCGGAGAGGTTAATTGAGGAACATCATCTCGGGCGGTGATACTGCCG  
SerTyrProAspAlaGluArgLeuIleGluGluThrSerTyrSerGlyValIleLeuPro 213  
#4  
CGGGTGCAATGCGCGCTTACCTACTACAACACGACCTGCACGACCTTGTGCCGTCCGCGG  
ArgValGlnCysAlaValThrTyrTyrAsnThrThrCysThrThrPheCysArgProArg 253  
TGGCAGGGCGTCAACTGCGAGGAGGCCATATGCAAGGCGGGCTGCGACCCCGTCCACGGC  
TrpGlnGlyValAsnCysGluGluAlaIleCysLysAlaGlyCysAspProValHisGly 293

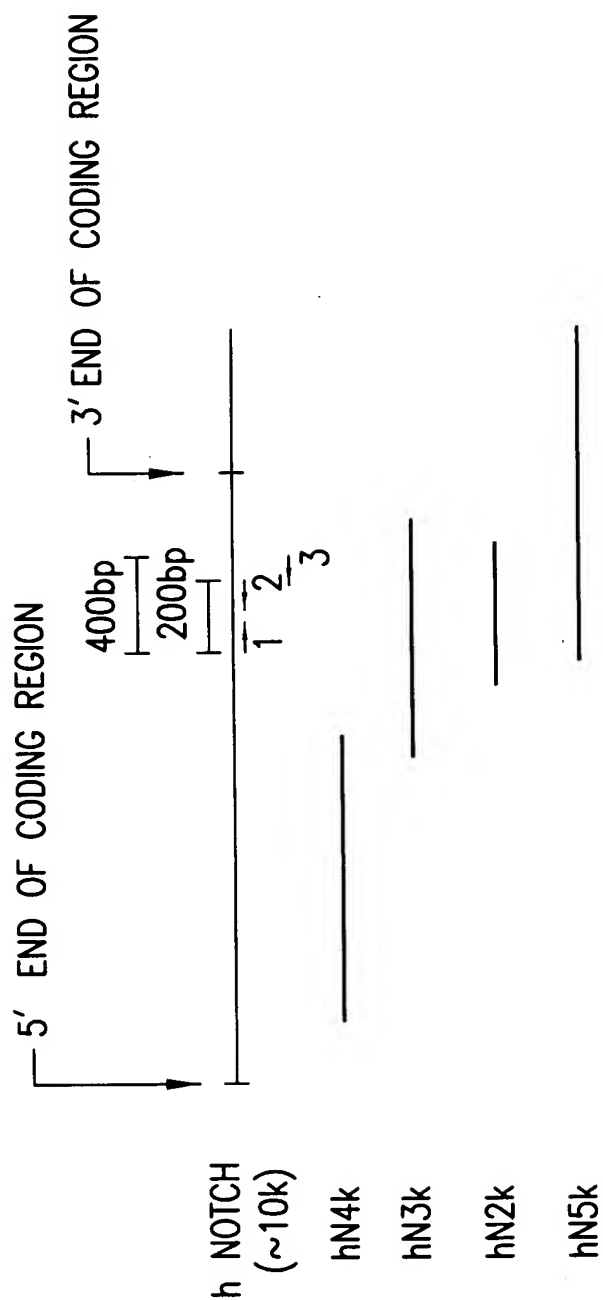
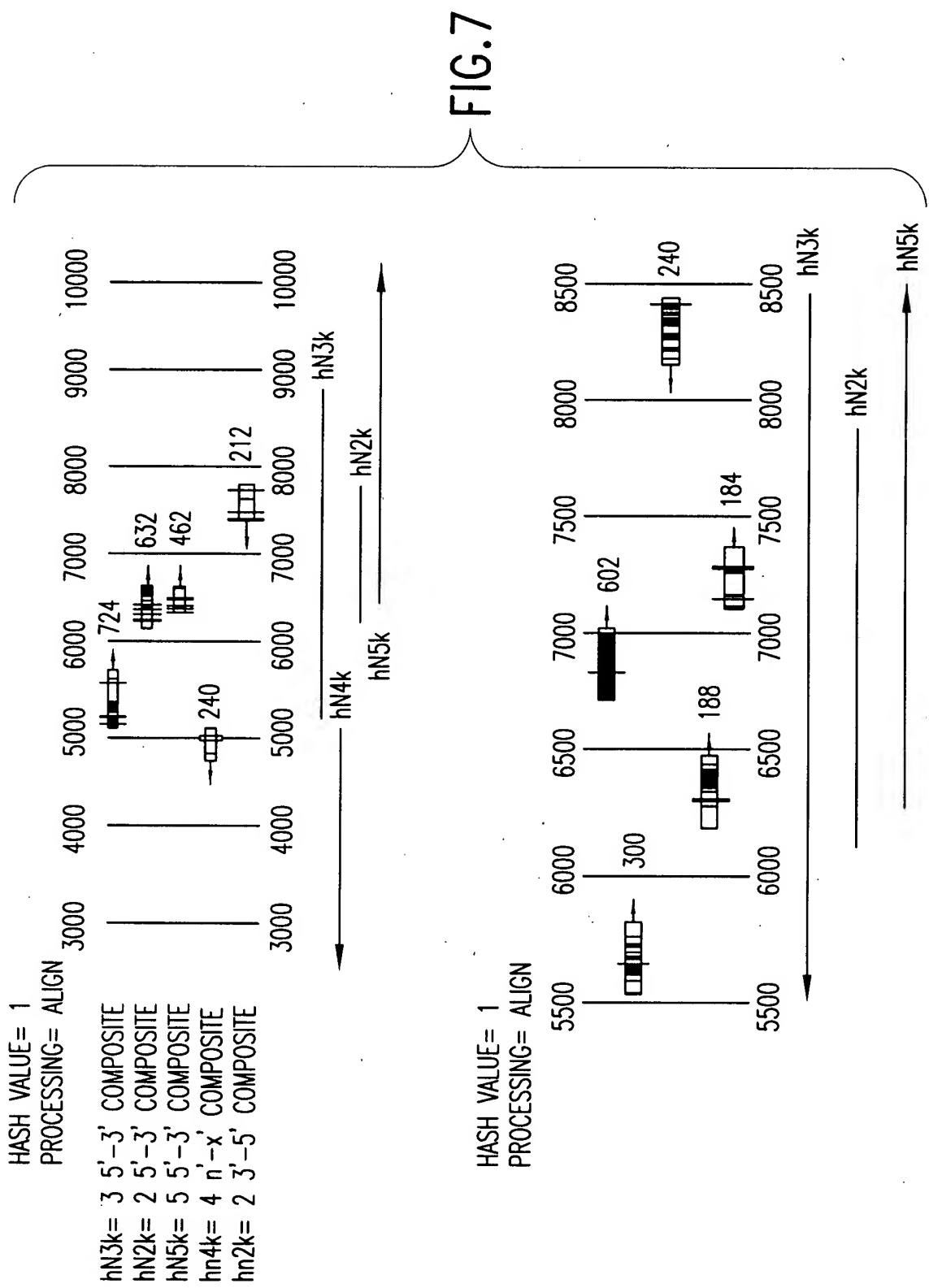


FIG.6



1 GAATTCGGCT GGGAGAATGG TCTGAGCTAC CTGCCCCTCC TGCTGGGGCA TCAATGGCAA  
61 GTGGGGAAAG CCACACTGGG CAAACGGGCC AGGCCATTTC TGAATGTGG TACATGGTGG  
121 GCAGGGGGCC CGCAACAGCT GGAGGGCAGG TGGACTGAGG CTGGGGATCC CCCGCTGGTT  
181 GGGCAATACT GCCTTTACCC ATGAGCTGGA AAGTCACAAT GGGGGGCAAG GGCTCCCAG  
241 GGTGGTTATG TGCTTCCTTC AGGTGGC

## FIG.8A

1 GAATTCCTTC CATTATACGT GACTTTTCTG AACTGTAGC CACCCTAGTG TCTCTAACTC  
61 CCTCTGGAGT TTGTCAGCTT TGGTCTTTTC AAAGAGCAGG CTCTCTTCAA GTCCTTAAT  
121 GCGGGCATGC TCCAGTTTGG TCTGCGTCTC AAGATCACCT TTGGTAATTG ATTCTTCTTC  
181 AACCCGGAAC TGAAGGCTGG CTCTCACCT CTAGGCAGAG CAGGAATTCC GAGGTGGATG  
241 TGTTAGATGT GAATGTCCGT GGCCAGATG GCTGCACCCC ATTGATGTTG GCTTCTCTCC  
301 GAGGAGGCAG CTCAGATTG AGTGATGAAG ATGAAGATGC AGAGGACTGT TCTGCTAACA  
361 TCATCACAGA CTTGGTCTAC CAGGGTGCCA GCCTCCAGAC CAGACAGACC GGAAGGTGA  
421 GATGGCCCTG CACCTTGCA GCGGCTACTC ACGGGCTGAT GCTGCCAAGC GTCTCCTGGA  
481 TGCAGGTGCA GATGCCAATG CCCAGGACAA CATGGGCGC TGTCCACTCC ATGCTGCAGT  
541 GGCACGTGAT GCCAAGGTGT ATTCAGATCT GTTA

## FIG.8B

1 TCCAGATTCT GATTGCAAC CGAGTAACTG ATCTAGATGC CAGGATGAAT GATGGTACTA  
61 CACCCCTGAT CCTGGCTGCC CGCCTGGCTG TGGAGGGAAT GGTGGCAGAA CTGATCAACT  
121 GCCAAGCGGA TGTGAATGCA GTGGATGACC ATGGAAAATC TGCTCTTAC TGGGCAGCTG  
181 CTGTCAATAA TGTGGAGGCA ACTCTTTTGT TGTGAAAAA TGGGGCCAAC CGAGACATGC  
241 AGGACAACAA GGAAGAGACA CCTCTGTTTC TTGCTGCCCCG GGAGGAGCTA TAAGC

## FIG.8C

1 GAATTCCATT CAGGAGGAAA GGGTGGGGAG AGAAGCAGGC ACCCACTTTC CCGTGGCTGG  
61 ACTCGTTCCT AGGTGGCTCC ACCGGCAGCT GTGACCGCCG CAGGTGGGGG CGGAGTGCCA  
121 TTCAGAAAAT TCCAGAAAAG CCCTACCCCA ACTCGGACGG CAACGTCACA CCCGTGGGTA  
181 GCAACTGGCA CACAAACAGC CAGCGTGTCT GGGGCACGGG GGGATGGCAC CCCCTGCAGG  
241 CAGAGCTG

## FIG.9A

1 CTAAAGGGAA CAAAAGCNGG AGCTCCACCG CGGGCGGCNC NGCTCTAGAA CTAGTGGANN  
61 NCCCGGGCTG CAGGAATTCC GGGGACTGG GCTCGGGCTC AGAGCGGCGC TGTGGAAGAG  
121 ATTCTAGACC GGGAGAACAA GCGAATGGCT GACAGCTGGC CTCCAAAGTC ACCAGGCTCA  
181 AATCGCTCGC CCTGGACATC GAGGGATGCA GAGGATCAGA ACCGGTACCT GGATGGCATG  
241 ACTCGGATTT ACAAGCATGA CCAGCCTGCT TACAGGGAGC GTGANNTTTT CACATGCAGT  
301 CGACAGACAC GAGCTCTATG CAT

## FIG.9B



10	20	30	40
* TGC CAG GAG GAC GCG GGC AAC AAG GTC TGC AGC CTG CAG TGC AAC AAC	* * * *	* * * *	* * * *
C Q E D A G N K V C S L Q C N N>			
50	60	70	80
* * * *	* * * *	* * * *	* * * *
CAC GCG TGC GGC TGG GAC GGC GGT GAC TGC TCC CTC AAC TTC AAT GAC			
H A C G G W D G G D C S L N F N D>			
100	110	120	130
* * * *	* * * *	* * * *	* * * *
CCC TGG AAG AAC TGC ACG CAG TCT CTG CAG TGC TGG AAG TAC TTC AGT			
P W K N C T Q S L Q C C W K Y F S>			
150	160	170	180
* * * *	* * * *	* * * *	* * * *
GAC GGC CAC TGT GAC AGC CAG TGC AAC TCA GCC GGC TGC CTC TTC GAC			
D G H C D S Q C N S A G C L F D>			

FIG. 10A

390	400	410	420	430
* CCG GAG CAG CTG	* AAC AGC TTC	* CAC TTC	* CTG CGG	* GAG CTC AGC
P E Q L R N S	S F H F L R E L S>			
440	450	460	470	480
* CCG GTG CAC ACC AAC GTG	* TTC AAG CGT	* GAC GCA	* CAC GGC	* CAG
R V L H T N V	F K R D A H G Q>			
490	500	510	520	
* CAG ATG ATC TTC CCC	* TAC TAC GGC	* CGC GAG	* CTG CGC	* AAG CAC
Q M I F P Y Y	G R E E L R K H>			
530	540	550	560	570
* CCC ATC AAG CGT	* GCC GGC	* TGG GCC	* GCA CCT	* GAC GCC
P I K R A A E	G W A A P D A L L>			

FIG. 10C

```

580      *      *      *      *      *      *      *      *      *      *
      GGC CAG GTG AAG GCC TCG CTG CTC CTC CCT GGT GGC AGC GAG GGT GGG CGG
      G  Q  V  K  A  S  L  L  L  L  L  L  L  L  L  L  L  L  L  L  L  L  L  L
      *      *      *      *      *      *      *      *      *      *
630      *      *      *      *      *      *      *      *      *      *
      CGG CCG AGG GAG CTG GAC CCC ATG GAC GTC CGC GGC TCC ATC GTC TAC
      R  R  R  E  L  L  D  P  M  D  V  R  G  S  I  V  Y>
      *      *      *      *      *      *      *      *      *      *
680      *      *      *      *      *      *      *      *      *      *
      CTG GAG ATT GAC AAC CCG CAG TGT GTG CAG GCC TCC TCG CAG TGC TTC
      L  E  I  D  N  R  Q  C  V  Q  A  S  S  Q  C  F>
      *      *      *      *      *      *      *      *      *      *
730      *      *      *      *      *      *      *      *      *      *
      CAG AGT GCC ACC GAC GTG GCC GCA TTC CTG GGA GCG CTC GCC TCG CTG
      Q  S  A  T  D  V  A  A  F  L  G  A  L  A  S  L>

```

FIG. 10D

**FIG. 10E**

970	980	990	1000
* * *	* *	* *	*
AAA GTG TCT GAG GCC AGC AAG AAG AAG CGG CGG GAG CCC CTC GGC GAG			
K V S E A S K K K R R E P L G E>			
1010	1020	1030	1040
* *	* *	* *	*
GAC TCC GTG GGC CTC AAG CCC CTG AAG AAC GCT TCA GAC GGT GCC CTC			
D S V G L K P L K N A S D G A L>			
1060	1070	1080	1090
* *	* *	* *	*
ATG GAC GAC AAC CAG AAT GAG TGG GGG GAC GAG CTG GAG ACC AAG			
M D D N Q N E W G D E D L E T K>			
1110	1120	1130	1140
* *	* *	* *	*
AAG TTC CGG TTC GAG GAG CCC GTG GTT CTG CCT GAC CTG GAC GAC CAG			
K F R F E E P V V L P D L D D Q>			

FIG.10F

1160	1170	1180	1190	1200
* * *	* *	* *	* *	* *
ACA GAC CAC CGG CAG TGG ACT CAG CAC CTG GAT GCC GCT GAC CTG				
T D H R Q Q W T Q Q H L D A A D L>				
1210	1220	1230	1240	
* * *	* *	* *	* *	
CGC ATG TCT GCC ATG GCC CCC ACA CCG CCC CAG GGT GAG GTT GAC GCC				
R M S A A M A P T P P Q G E V D A>				
1250	1260	1270	1280	1290
* * *	* *	* *	* *	* *
GAC TGC ATG GAC GTC AAT GTC CGC GGG CCT GAT GGC TTC ACC CCG CTC				
D C M D V N V R G P D G F T P L>				
1300	1310	1320	1330	1340
* * *	* *	* *	* *	* *
ATG ATC GCC TCC TGC AGC GGC GGC GGC CTG GAG ACG GGC AAC AGC GAG				
M I A S C S G G G L E T G N S E>				

FIG.10G

1350	1360	1370	1380	1390
* GAA GAG GAG GAC GCG CCG GCC GTC ATC TTC GAC TTC ATC TAC CAG GGC	* * * *	* * * *	* * * *	* * * *
E E E D A P A V I S D F I Y Q G>				
1400	1410	1420	1430	1440
* GCC AGC CTG CAC AAC CAG ACA GAC CGC ACG GGC GAG ACC GCC TTG CAC	* * * *	* * * *	* * * *	* * * *
A S L H N Q T D R T G E T A L HD>				
1450	1460	1470	1480	
* CTG GCC GCC CGC TAC TCA CGC TCT GAT GCC GCC AAG CGC CTG CTG GAG	* * * *	* * * *	* * * *	
L A A R Y S R S D A A K R L E>				
1490	1500	1510	1520	1530
* GCC AGC GCA GAT GCC AAC ATC CAG GAG AAC ATG GGC CGC ACC CCG CTG	* * * *	* * * *	* * * *	* * * *
A S A D A N I Q D N M G R T P L>				

FIG. 10H

1540	1550	1560	1570	1580
* CAT GCG GCT GTG TCT GCC GAC GCA CAA GGT GTC TTC CAG ATC CTG ATC	* H A A V S A D A Q G V F Q I L I>			
1590	1600	1610	1620	1630
* CGG AAC CGA GCC ACA GAC CTG GAT GCC CGC ATG CAT GAT GGC ACG ACG	* R N R A T D L D A R M H D G T T>			
1640	1650	1660	1670	1680
* CCA CTG ATC CTG GCT GCC CGC CTG GAT GCC GTG GAG GGC ATG CTG GAG GAC	* P L I L A A R L A V E G M L E D>			
1690	1700	1710	1720	
* CTC ATC AAC TCA CAC GCC GAC GTC AAC GCC GTA GAT GAC CTG GGC AAG	* L I N S H A D V N A V D D L G K>			
1730	1740	1750	1760	1770
* TCC GCC CTG CAC TGG GCC GCC GTC AAC AAT GTG GAT GCC GCA GTT	* S A L H W A A A V N N V D A A V>			

FIG. 10I



1780	1790	1800	1810	1820
* GTG CTC CTG AAG AAC GGG GCT AAC AAA GAT ATG CAG AAC AAC AGG GAG	* * * * *	* * * * *	* * * * *	* * * * *
V L L K N G A N K D M Q N R E>				
1830	1840	1850	1860	1870
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
GAG ACA CCC CTG TTT CTG GCC GCC CGG GAG GGC AGC TAC GAG ACC GCC				
E T P L F L A A R E G S Y E T A>				
1880	1890	1900	1910	1920
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *
AAG GTG CTG CTG GAC CAC TTT GCC AAC CGG GAC ATC ACG GAT CAT ATG				
K V L L D H F A N R D I T D H M>				
1930	1940	1950	1960	
* * * * *	* * * * *	* * * * *	* * * * *	
GAC CGC CTG CCG CGC GAC ATC GCA CAG GAG CGC ATG CAT CAC GAC ATC				
D R L P R D I A Q E R M H D I>				

FIG.10J

1970	1980	1990	2000	2010	
* GTG AGG CTG CTG GAC GAG TAC AAC CTG GTG CGC AGC CCG CAG CTG CAC	* * *	* *	* *	* *	*
V R L L D E Y N L V R S P Q L H>					
2020	2030	2040	2050	2060	
* * *	* *	* *	* *	*	
GGA GCC CCG CTG GGG GGC AGC ACC CTG TCG CCC CCG CTC TGC TCG					
G A P L G G T P T L S P P L C S>					
2070	2080	2090	2100	2110	
* * *	* *	* *	* *	*	
CCC AAC GGC TAC CTG GGC AGC CTC AAG CCC GGC GTG CAG GGC AAG AAG					
P N G Y L L G S L K P P V Q G K K>					
2120	2130	2140	2150	2160	
* * *	* *	* *	* *	*	
GTC CGC AAG CCC AGC AGC AAA GGC CTG GCC TGT GGA AGC AAG GAG GCC					
V R K P S S K G G L A C G S K E A>					

FIG. 10K

2170	2180	2190	2200
* AAG GAC CTC AAG GCA CGG AGG AAG AAG TCC CAG GAT GGC AAG GGC TGC	* *	* *	* *
K D L K A R R K K S Q D G K G C>			
2210	2220	2230	2240
* CTG CTG GAC AGC TCC GGC ATG CTC TCG CCC GTG GAC TCC CTG GAG TCA	* *	* *	* *
L L D S S G M L S P V D S L E S>			
2260	2270	2280	2290
* CCC CAT GGC TAC CTG TCA GAC GTG GCC TCG CCG CCA CTG CTG CCC TCC	* *	* *	* *
P H G Y L S D V A S P P L P S>			
2310	2320	2330	2340
* CCG TTC CAG CAG TCT CCG TCC GTG CCC CTC AAC CAC CTG CCT GGG ATG	* *	* *	* *
P F Q Q S S P S V P L N H L P G M>			

FIG.10L

2550	2560	2570	2580	2590
* ACC AGT TTG AAT GGT CAA TGC GAG TGG CTG TCC CGG CTG CAG AGC GGC	*	*	*	*
T S L N G Q C E W L S R L Q S G>				
2600	2610	2620	2630	2640
* ATG GTG CCG AAC CAA TAC AAC CCT CTG CCG GGG AGT GTG GCA CCA GGC	*	*	*	*
M V P N Q Y N P L R G S V A P G>				
2650	2660	2670	2680	
* CCC CTG AGC ACA CAG GCC CCC TCC CTG CAG CAT GGC ATG GTA GGC CCG	*	*	*	*
P L S T Q A P S L Q H G M V G P>				
2690	2700	2710	2720	2730
* CTG CAC AGT AGC CTT GCT GCC AGC GCC CTG TCC CAG ATG ATG AGC TAC	*	*	*	*
L H S S L A A S A L S Q M M S Y>				

FIG. 10N

2360	2370	2380	2390	2400
* CCC GAC ACC CAC CTG GGC ATC GGG CAC CTG AAC GTG GCG GCC AAG CCC				
P D T H L G I G H L N V A A K P>				
	2410	2420	2430	2440
	* GAG ATG GCG GCG CTG GGT GGG GGC GGC CTG GCG TTT GAG ACT GGC			
E M A A L G G G G G R L A F E T G>				
2450	2460	2470	2480	2490
* CCA CCT CGT CTC TCC CAC CTG CCT CTG GCG TCT GCG ACC AGC ACC GTC				
P P R L S H L P V A S G T S T V>				
2500	2510	2520	2530	2540
* CTG GGC TCC AGC AGC GGA GGG GCG CTG AAT TTC ACT GTG GCG GGG TCC				
L G S S S G G A L N F T V G G S>				

FIG.10M

2740	2750	2760	2770	2780
* CAG GGC CTG CCC AGC ACC CGG CTG GCC ACC CAG CCT CAC CTG GTG CAG Q G L P S T R L A T Q P H L V Q>	* 2750	* 2760	* 2770	* 2780
2790	2800	2810	2820	2830
* ACC CAG CAG GTG CAG CCA CAA AAC TTA CAG ATG CAG CAG AAC CTG T Q Q V Q P Q Q N L Q M Q Q N L>	* 2800	* 2810	* 2820	* 2830
2840	2850	2860	2870	2880
* CAG CCA GCA AAC ATC CAG CAG CAG CAA AGC CTG CAG CCG CCA CCA CCA Q P A N I Q Q Q Q S L Q P P P>	* 2850	* 2860	* 2870	* 2880
2890	2900	2910	2920	
* CCA CCA CAG CCG CAC CTT GGC GTG AGC TCA GCA GCC AGC GGC CAC CTG P P Q P H L G V S S A A S G H L>	* 2900	* 2910	* 2920	
2930	2940	2950	2960	2970
* GGC CGG AGC TTC CTG AGT GGA GAG CCG AGC CAG GCA GAC GTG CAG CCA G R S F L S G G E P S Q A D V Q P>	* 2940	* 2950	* 2960	* 2970

FIG.100

2980	2990	3000	3010	3020
CTG GGC CCC AGC AGC CTG GCG GTG CAC ACT ATT CTG CCC CAG GAG AGC				
L G P S S L A V H T I L P Q E S>				
3030	3040	3050	3060	3070
CTG GGC CTG CCC ACG TCG TCG CTG CCA TCC TCG CTG GTC CCA CCC GTG ACC				
P A L P T S S L P S S L V P P V T>				
3080	3090	3100	3110	3120
GCA GCC CAG TTC CTG ACG CCC CCC TCG CAG CAC AGC TAC TCC TCG CCT				
A A Q F L T P P S Q H S Y S P>				

FIG. 10P

3130	3140	3150	3160	
* GTG GAC AAC ACC CCC AGC CAC CAG CTA CAG GTG CCT GTT CCT GTA ATG	* *	* *	* *	*
V D N T P S H Q L Q V P V P V M>				
3170	3180	3190	3200	3210
* GTA ATG ATC CGA TCT TCG GAT CCT TCT AAA GGC TCA ATT TTG ATC	* *	* *	* *	*
V M I R S S D P S S I L				
3220	3230			
* GAA GCT CCC GAC TCA TGG	* *			
E A P D S W>				

FIG.10Q



G GAG GTG GAT GTG TTA GAT GTG AAT GTC CGT GGC CCA GAT GGC TGC Glu Val Asp Val Leu Asp Val Asn Val Arg Gly Pro Asp Gly Cys 1 5 10 15	46
ACC CCA TTG ATG TTG GCT TCT CTC CGA GGA GGC AGC TCA GAT TTG AGT Thr Pro Leu Met Leu Ala Ser Leu Arg Gly Gly Ser Ser Asp Leu Ser 20 25 50	94
GAT GAA GAT GAA GAT GCA GAG GAC TCT TCT GCT AAC ATC ATC ACA GAC Asp Glu Asp Glu Asp Ala Glu Asp Ser Ser Ala Asn Ile Ile Thr Asp 35 40 45	142
TTG GTC TAC CAG GGT GCC AGC CTC CAG GCC CAG ACA GAC CGG ACT GGT Leu Val Tyr Gln Gly Ala Ser Leu Gln Ala Gln Thr Asp Arg Thr Gly 50 55 60	190
GAG ATG GCC CTG CAC CTT GCA GCC CGC TAC TCA CGG GCT GAT GCT GCC Glu Met Ala Leu His Leu Ala Ala Arg Tyr Ser Arg Ala Asp Ala Ala 65 70 75	238
AAG CGT CTC CTG GAT GCA GGT GCA GAT GCC AAT GCC CAG GAC AAC ATG Lys Arg Leu Leu Asp Ala Gly Ala Asp Ala Asn Ala Gln Asp Asn Met 80 85 90 95	286
GGC CGC TGT CCA CTC CAT GCT GCA GTG GCA GCT GAT GCC CAA GGT GTC Gly Arg Cys Pro Leu His Ala Ala Val Ala Ala Asp Ala Gln Gly Val 100 105 110	334
TTC CAG ATT CTG ATT CGC AAC CGA GTA ACT GAT CTA GAT GCC AGG ATG Phe Gln Ile Leu Ile Arg Asn Arg Val Thr Asp Leu Asp Ala Arg Met 115 120 125	382
AAT GAT GGT ACT ACA CCC CTG ATC CTG GCT GCC CGC CTG GCT GTG GAG Asn Asp Gly Thr Thr Pro Leu Ile Leu Ala Ala Arg Leu Ala Val Glu 130 135 140	430

FIG.11A

GGA ATG GTG GCA GAA CTG ATC AAC TGC CAA GCG GAT GTG AAT GCA GTG	478
Gly Met Val Ala Glu Leu Ile Asn Cys Gln Ala Asp Val Asn Ala Val	
145 150 155	
GAT GAC CAT GGA AAA TCT GCT CTT CAC TGG GCA GCT GCT GTC AAT AAT	526
Asp Asp His Gly Lys Ser Ala Leu His Trp Ala Ala Ala Val Asn Asn	
160 165 170 175	
GTG GAG GCA ACT CTT TTG TTG TTG AAA AAT GGG GCC AAC CGA GAC ATG	574
Val Glu Ala Thr Leu Leu Leu Lys Asn Gly Ala Asn Arg Asp Met	
180 185 190	
CAG GAC AAC AAG GAA GAG ACA CCT CTG TTT CTT GCT GCC CGG GAG GGG	622
Gln Asp Asn Lys Glu Glu Thr Pro Leu Phe Leu Ala Ala Arg Glu Gly	
195 200 205	
AGC TAT GAA GCA GCC AAG ATC CTG TTA GAC CAT TTT GCC AAT CGA GAC	670
Ser Tyr Glu Ala Ala Lys Ile Leu Leu Asp His Phe Ala Asn Arg Asp	
210 215 220	
ATC ACA GAC CAT ATG GAT CGT CTT CCC CGG GAT GTG GCT CGG GAT CGC	718
Ile Thr Asp His Met Asp Arg Leu Pro Arg Asp Val Ala Arg Asp Arg	
225 230 235	
ATG CAC CAT GAC ATT GTG CGC CTT CTG GAT GAA TAC AAT GTG ACC CCA	766
Met His His Asp Ile Val Arg Leu Leu Asp Glu Tyr Asn Val Thr Pro	
240 245 250 255	
AGC CCT CCA GGC ACC GTG TTG ACT TCT GCT CTC TCA CCT GTC ATC TGT	814
Ser Pro Pro Gly Thr Val Leu Thr Ser Ala Leu Ser Pro Val Ile Cys	
260 265 270	
GGG CCC AAC AGA TCT TTC CTC AGC CTG AAG CAC ACC CCA ATG GGC AAG	862
Gly Pro Asn Arg Ser Phe Leu Ser Leu Lys His Thr Pro Met Gly Lys	
275 280 285	

FIG.11B

AAG TCT AGA CGG CCC AGT GCC AAG AGT ACC ATG CCT ACT AGC CTC CCT	910
Lys Ser Arg Arg Pro Ser Ala Lys Ser Thr Met Pro Thr Ser Leu Pro	
290 295 300	
AAC CTT GCC AAG GAG GCA AAG GAT GCC AAG GGT AGT AGG AGG AAG AAG	958
Asn Leu Ala Lys Glu Ala Lys Asp Ala Lys Gly Ser Arg Arg Lys Lys	
305 310 315	
TCT CTG AGT GAG AAG GTC CAA CTG TCT GAG AGT TCA GTA ACT TTA TCC	1006
Ser Leu Ser Glu Lys Val Gln Leu Ser Glu Ser Ser Val Thr Leu Ser	
320 325 330 335	
CCT GTT GAT TCC CTA GAA TCT CCT CAC ACG TAT GTT TCC GAC ACC ACA	1054
Pro Val Asp Ser Leu Glu Ser Pro His Thr Tyr Val Ser Asp Thr Thr	
340 345 350	
TCC TCT CCA ATG ATT ACA TCC CCT GGG ATC TTA CAG GCC TCA CCC AAC	1102
Ser Ser Pro Met Ile Thr Ser Pro Gly Ile Leu Gln Ala Ser Pro Asn	
355 360 365	
CCT ATG TTG GCC ACT GCC GCC CCT CCT GCC CCA GTC CAT GCC CAG CAT	1150
Pro Met Leu Ala Thr Ala Ala Pro Pro Ala Pro Val His Ala Gln His	
370 375 380	
GCA CTA TCT TTT TCT AAC CTT CAT GAA ATG CAG CCT TTG GCA CAT GGG	1198
Ala Leu Ser Phe Ser Asn Leu His Glu Met Gln Pro Leu Ala His Gly	
385 390 395	
GCC AGC ACT GTG CTT CCC TCA GTG AGC CAG TTG CTA TCC CAC CAC CAC	1246
Ala Ser Thr Val Leu Pro Ser Val Ser Gln Leu Leu Ser His His His	
400 405 410 415	
ATT GTG TCT CCA GGC AGT GGC AGT GCT GGA AGC TTG AGT AGG CTC CAT	1294
Ile Val Ser Pro Gly Ser Gly Ser Ala Gly Ser Leu Ser Arg Leu His	
420 425 430	
CCA GTC CCA GTC CCA GCA GAT TGG ATG AAC CGC ATG GAG GTG AAT GAG	1342
Pro Val Pro Val Pro Ala Asp Trp Met Asn Arg Met Glu Val Asn Glu	
435 440 445	

FIG.11C

ACC CAG TAC AAT GAG ATG TTT GGT ATG GTC CTG GCT CCA GCT GAG GGC	1390
Thr Gln Tyr Asn Glu Met Phe Gly Met Val Leu Ala Pro Ala Glu Gly	
450 455 460	
ACC CAT CCT GGC ATA GCT CCC CAG AGC AGG CCA CCT GAA GGG AAG CAC	1438
Thr His Pro Gly Ile Ala Pro Gln Ser Arg Pro Pro Glu Gly Lys His	
465 470 475	
ATA ACC ACC CCT CGG GAG CCC TTG CCC CCC ATT GTG ACT TTC CAG CTC	1486
Ile Thr Thr Pro Arg Glu Pro Leu Pro Pro Ile Val Thr Phe Gln Leu	
480 485 490 495	
ATC CCT AAA GGC AGT ATT GCC CAA CCA GCG GGG GCT CCC CAG CCT CAG	1534
Ile Pro Lys Gly Ser Ile Ala Gln Pro Ala Gly Ala Pro Gln Pro Gln	
500 505 510	
TCC ACC TGC CCT CCA GCT GTT GCG GGC CCC CTG CCC ACC ATG TAC CAG	1582
Ser Thr Cys Pro Pro Ala Val Ala Gly Pro Leu Pro Thr Met Tyr Gln	
515 520 525	
ATT CCA GAA ATG GCC CGT TTG CCC AGT GTG GCT TTC CCC ACT GCC ATG	1630
Ile Pro Glu Met Ala Arg Leu Pro Ser Val Ala Phe Pro Thr Ala Met	
530 535 540	
ATG CCC CAG CAG GAC GGG CAG GTA GCT CAG ACC ATT CTC CCA GCC TAT	1678
Met Pro Gln Gln Asp Gly Gln Val Ala Gln Thr Ile Leu Pro Ala Tyr	
545 550 555	
CAT CCT TTC CCA GCC TCT GTG GGC AAG TAC CCC ACA CCC CCT TCA CAG	1726
His Pro Phe Pro Ala Ser Val Gly Lys Tyr Pro Thr Pro Pro Ser Gln	
560 565 570 575	
CAC AGT TAT GCT TCC TCA AAT GCT GCT GAG CGA ACA CCC AGT CAC AGT	1774
His Ser Tyr Ala Ser Ser Asn Ala Ala Glu Arg Thr Pro Ser His Ser	
580 585 590	
GGT CAC CTC CAG GGT GAG CAT CCC TAC CTG ACA CCA TCC CCA GAG TCT	1822
Gly His Leu Gln Gly Glu His Pro Tyr Leu Thr Pro Ser Pro Glu Ser	
595 600 605	

FIG.11D

CCT GAC CAG TGG TCA AGT TCA TCA CCC CAC TCT GCT TCT GAC TGG TCA Pro Asp Gln Trp Ser Ser Ser Ser Pro His Ser Ala Ser Asp Trp Ser 610 615 620	1870
GAT GTG ACC ACC AGC CCT ACC CCT GGG GGT GCT GGA GGA GGT CAG CCG Asp Val Thr Thr Ser Pro Thr Pro Gly Gly Ala Gly Gly Gly Gln Arg 625 630 635	1918
GGA CCT GGG ACA CAC ATG TCT GAG CCA CCA CAC AAC AAC ATG CAG GTT Gly Pro Gly Thr His Met Ser Glu Pro Pro His Asn Asn Met Gln Val 640 645 650 655	1966
TAT GCG TGAGAGAGTC CACCTCCAGT GTAGAGACAT AACTGACTTT TGTAATGCT Tyr Ala	2022
GCTGAGGAAC AAATGAAGGT CATCCGGGAG AGAAATGAAG AAATCTCTGG AGCCAGCTTC	2082
TAGAGGTAGG AAAGAGAAGA TGTTCCTATT CAGATAATGC AAGAGAAGCA ATTCGTCAGT	2142
TTCACTGGGT ATCTGCAAGG CTTATTGATT ATTCTAATCT AATAAGACAA GTTTGTGGAA	2202
ATGCAAGATG AATACAAGCC TTGGGTCCAT GTTTACTCTC TTCTATTTGG AGAATAAGAT	2262
GGATGCTTAT TGAAGCCCAG ACATTCTTGC AGCTTGGACT GCATTTTAAG CCCTGCAGGC	2322
TTCTGCCATA TCCATGAGAA GATTCTACAC TAGCGTCCTG TTGGGAATTA TGCCCTGGAA	2382
TTCTGCCTGA ATTGACCTAC GCATCTCCTC CTCCTTGGAC ATTCTTTTGT CTTCAATTGG	2442
TGCTTTTGGT TTTGCACCTC TCCGTGATTG TAGCCCTACC AGCATGTTAT AGGGCAAGAC	2502
CTTTGTGCTT TTGATCATTG TGGCCCATGA AAGCAACTTT GGTCTCCTTT CCCCTCCTGT	2562
CTTCCCGGTA TCCCTTGGAG TCTCACAAGG TTTACTTTGG TATGGTTCTC AGCACAACC	2622
TTTCAAGTAT GTTGTCTTCT TGGAAAATGG ACATACTGTA TTGTGTTCTC CTGCATATAT	2682
CATTCCTGGA GAGAGAAGGG GAGAAGAATA CTTTCTTCA ACAAATTTTG GGGCAGGAG	2742
ATCCCTTCAA GAGGCTGCAC CTTAATTTTT CTTGTCTGTG TGCAGGTCTT CATATAAAT	2802

FIG.11E

TTACCAGGAA GAAGGGTGTG AGTTTGTGT TTTTCTGTGT ATGGGCCTGG TCAGTGTA	2862
TTTATCCT TGATAGTCTA GTTACTATGA CCCTCCCCAC TTTTAAAA CCAGAAAAAG	2922
GTTTGAATG TTGGAATGAC CAAGAGACAA GTTAACTCGT GCAAGAGCCA GTTACCCACC	2982
CACAGGTCCC CCTACTTCCT GCCAAGCATT CCATTGACTG CCTGTATGGA ACACATTGT	3042
CCCAGATCTG AGCATTCTAG GCCTGTTTCA CTCACTCACC CAGCATATGA AACTAGTCTT	3102
AACTGTTGAG CCTTTCCTTT CATATCCACA GAAGACACTG TCTCAAATGT TGTACCCTTG	3162
CCATTTAGGA CTGAACTTTC CTTAGCCCAA GGGACCCAGT GACAGTTGTC TTCCGTTTGT	3222
CAGATGATCA GTCTCTACTG ATTATCTTGC TGCTTAAAGG CCTGCTCACC AATCTTTCTT	3282
TCACACCGTG TGGTCCGTGT TACTGGTATA CCCAGTATGT TCTCACTGAA GACATGGACT	3342
TTATATGTTT AAGTGCAGGA ATTGGAAAGT TGGACTTGTT TTCTATGATC CAAAACAGCC	3402
CTATAAGAAG GTTGGAAAAG GAGGAACTAT ATAGCAGCCT TTGCTATTTT CTGCTACCAT	3462
TTCTTTTCCT CTGAAGCGGC CATGACATTC CCTTTGGCAA CTAACGTAGA AACTCAACAG	3522

FIG.11F

AACATTTTCC TTTCTAGAG TCACCTTTTA GATGATAATG GACAACTATA GACTTGCTCA	3582
TTGTTGAGAC TGATTGCCCC TCACCTGAAT CCACTCTCTG TATTCATGCT CTTGGCAATT	3642
TCTTTGACTT TCTTTTAAGG GCAGAAGCAT TTTAGTTAAT TGTAGATAAA GAATAGTTTT	3702
CTTCCTCTTC TCCTTGGGCC AGTTAATAAT TGGTCCATGG CTACACTGCA ACTTCCGTCC	3762
AGTGCTGTGA TGCCCATGAC ACCTGCAAAA TAAGTTCTGC CTGGGCATTT TGTAGATATT	3822
AACAGGTGAA TTCCCGACTC TTTTGGTTTG AATGACAGTT CTCATTCCCT CTATGGCTGC	3882
AAGTATGCAT CAGTGCTTCC CACTTACCTG ATTTGTCTGT CGGTGGCCCC ATATGGAAAC	3942
CCTGCGTGTC TGTTGGCATA ATAGTTTACA AATGGTTTTT TCAGTCCTAT CCAAATTTAT	4002
TGAACCAACA AAAATAATTA CTCTGCCCT GAGATAAGCA GATTAAGTTT GTTCATTCTC	4062
TGCTTTATTC TCTCCATGTG GCAACATTCT GTCAGCCTCT TTCATAGTGT GCAAACATTT	4122
TATCATTCTA AATGGTGACT CTCTGCCCTT GGACCCATTT ATTATTCACA GATGGGGAGA	4182
ACCTATCTGC ATGGACCCTC ACCATCCTCT GTGCAGCACA CACAGTGCAG GGAGCCAGTG	4242
GCGATGGCGA TGACTTTCTT CCCCTG	4268

**FIG. 11G**

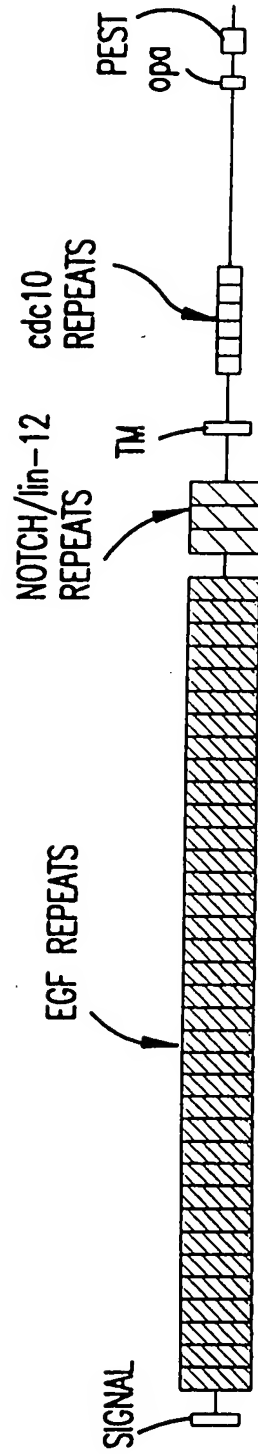


FIG.12A





CK-II

CK-11

[illegible]

SVAFPTAMPQQDQVAQTILPAYHPFASVCKYHTPPSQHSYASSNAAERTPSHSGHLQGEHPYLTPSPESPDQWSSSSPHSA-SDWSDVTTSPIT	
2448	SSLAVHTILPQ-ESPALPTSLPSSLVPPVTAAGFLTPPSQHSY-SS-PVENTPSHLQVLP-EHPFLTPSPESPDQWSSSSPHSNVSDWSEGVSSPPT
2423	SSLPVHTILPQ-ESQALPTSLPSSWVPPMTTTFLLTPPSQHSY-SSSPVDNTPSHLQVLP-EHPFLTPSPESPDQWSSSSRHSNISDWSEGLSSPPT
2416	SSNNIHSVMPQ-DTQIFAASLPNLTQSMTTAGFLTPPSQHSY-SS-PMNDNTPSHLQVLP-DHPFLTPSPESPDQWSSSSPHSNVSDWSEGLSSPPT
2599	S---IQSSMSG-SSPSTNMLSPSSQHNGQAFQYLLTPSSQHS-----GGHTPQHLVQTL-D-SYPTSPSPGHVSSSSPSRN-SDWSEGVQSPAA

## PEST-CONTAINING REGION

**FIG. 12C**

		Potential signal cleavage site									
hum N	MP	-----	-----	-----	ALRPAL	LWALLALWLC	CA	-----	APA	HA	-----
TAN-1	MP	-----	-----	-----	PL	LAPLLCLALL	PA	-----	LAA	RG	-----
Xen N	MD	-----	-----	-----		RIGLAVLLCS	LP	-----	VLT	QG	-----
Dros N	MQSQSRRRRS	RAPNTWICFW	INKMHAVASL	PASLPLLLLT	LAFANLPNIV	RGTDTALVAA					
hum N	MLGKATCRCA	SGFTGEDCQY	STSHPCFVSR	PCLNGGTCHM	LSRDT-YECT	CQVGFTGKEC					
Tan-1	GVADYACSCA	LGFSGPLCLT	PLDNAC-LTN	PCRNGGTCDL	LT-LTEYKCR	CPPGWSGKSC					
Xen N	NAIDFICHCP	VGFTDKVCLT	PVDNAC-VNN	PCRNGGTCEL	LNSVTEYKCR	CPPGWTGDSC					
Dros N	GRPGISCKCP	LGFDLSCEI	AVPNAC-DHV	TCLNGGTQCL	KT-LEETCA	CANGYTGERC					
hum N	NLPGSYQCQC	PQGFTGQYCD	SLYVPCAPSP	CVNGGTCRQT	GDFTFECNCL	PGFEGSTCER					
TAN-1	NEVGSYRCVC	RATHTGPNCE	RPYVPCSPSP	CQNGGTCRPT	GDVTHECACL	PGFTGQNCEE					
Xen N	NEFGSYRCTC	QNRFTGRNCD	EPYVPCNPSP	CLNGGTCRQT	DDTSYDCTCL	PGFSGQNCEE					
Dros N	NTHGSYQCMC	PTGYTGKDCD	TKYNPCSPSP	CQAGICRSN	G-LSYECKCP	KGFEGKNCEE					

#### EGF-like Repeats

QCRDGYEPCV	NEGMCVTYHN	GTGYCKPEG	FLGEYCQHRD	PCE-KNRCQN	GGTC-VAQA	83
RCSQPGETCL	NGGKCEA-AN	GTEACVCGGA	FVGPRCQDPN	PCL-STPCKN	AGTCHVDDR	80
RCTQTAEMCL	NGGRCEMPG	GTGVCLOGNL	YGERCQFPN	PCTIKNQCMN	FGTCEPVLQG	90
SCTSVG-CQ	NGGTCVTQLN	GKTYCACDSH	YVGDYCEHRN	PCN-SMRCQN	GGTCQVTFRN	117
QWTDACLSP	CANGSTCTTV	-ANQFSCKC	LTGFTGQKCE	TDVNEC-DIP	GHCQHGGTCL	199
QQADPCASNP	CANGGQCLPF	-EASYICHG	PPSFHGPTCR	QDVNECGQKP	RLCRHGGTCH	196
QQADPCASNP	CANGGKCLPF	-EIQYICKC	PPGFHGATCK	QDINEC-S-Q	NPCKNGGQC	195
ETKNLCASSP	CRNGATCTAL	AGSSSFCTSC	PPGFTGDTCS	YDIEEC-Q-S	NPCKYGGICV	233
NIDDCPNHRC	QNGGVCVDGV	NTYNCRCPPO	WTGQFCTEDV	DECLLPNA-	CQNGGTCANR	318
NIDDCPGNNC	KNGGACVDGV	NTYNCPPE	WTGQYCTEDV	DECQLMPNA-	CQNGGTCNNT	315
NIDDCPSNNC	RNGGTCVDGV	NTYNCCPPD	WTGQYCTEDV	DECQLMPNA-	CQNGGTCNNT	314
NYDDCLGHLC	QNGGTCIDGI	SDYTCRCPPN	FTGRFCQDDV	DECAQRDHPV	CQNGATCTNT	352

FIG.13A

hum N	NGGYGCVN	GWGDDCSEN	IDDCAFASCT	PGSTCIDRVA	SFSCMCPECK	AGLLCHLDDA
TAN-1	HGGYNVCVN	GWTGEDCSEN	IDDCASAACT	HGATCHDRVA	SFYCECPHGR	TGLLCHLNDA
Xen N	YGGYNVCVN	GWTGEDCSEN	IDDCANAACH	SGATCHDRVA	SFYCECPHGR	TGLLCHLDNA
Dros N	HGSYSICVN	GWAGLDCSNN	TDDCKQAACF	YGATCIDGVG	SFYCQCTKGG	TGLLCHLDDA

hum N	AFHCECLKGY	AGPRCEMDIN	ECHSDPCQND	ATCLDKIGGF	TCLCMPGFKG	VHCELEINEC
TAN-1	SFECQCLQGY	TGPRCEIDVN	ECVSNPCQND	ATCLDQIGEF	QCMCMGYEG	VHCEVNTDEC
Xen N	SFQCNCQGY	AGPRCEIDVN	ECLSNPCQND	STCLDQIGEF	QCICMPGYEG	LYCETNIDEC
Dros N	SYRCNCSQGF	TGPRCETNIN	ECESHPCQNE	GSLDDPGTF	RCVCMGFTG	TQCEIDIDEC

hum N	ATGFTGVLCE	ENIDNCDPDP	CHHGQCQDGI	DSYTCICNPG	YMGATCSDQI	DECYSSPCLN
TAN-1	TEGYTGTHCE	VDIDECDDP	CHYGSKDGV	ATFTCLCRPG	YTGHHCETNI	NECSSQPCRL
Xen N	TEGFTGRHCE	QDINECIPDP	CHYGTCKDGI	ATFTCLCRPG	YTGRLCDNDI	NECLSKPCLN
Dros N	PPGYGTSC	ININDCDSNP	CHRGKCIDDV	NSFKCLCDPG	YTGYYCQKQI	NECESNPCQF

CISNPCHKGA	LCDTNPLNGQ	YICTCPQGYK	GADCTEDVDE	CAMANSNPCE	HAGKCVNTDG	438
CISNPCNEGS	NCDTNPVNGK	AICTCPSGYT	GPACSQDVDE	CSLG-ANPCE	HAGKCINTLG	434
CISNPCNEGS	NCDTNPVNGK	AICTCPPGYT	GPACNNDVDE	CSLG-ANPCE	HGGRCNTNLG	433
CTSNPCHADA	ICDTSPINGS	YACSCATGYK	GVDCSEIDDE	CDQG-SPCE	HNGICVNTPG	470

QSNPCVNNGQ	CVDKVNRFQC	LCPPGFTGPV	CQIDIDDCSS	TPCLNGAKCI	DHPNGYECQC	558
ASSPCLHNGR	CLDKINEFQC	ECPTGFTGHL	CQYDVECAS	TPCKNGAKCL	DGPNTYTCVC	554
ASNPCLHNGK	CIDKINEFRC	DCPTGFSGNL	CQHDFDECTS	TPCKNGAKCL	DGPNSYTCQC	553
QSNPCLNDGT	CHDKINGFKC	SCALGFTGAR	CQINIDDCQS	QPCRNRGICH	DSIAGYSCEC	590

DGRCIDLUNG	YQCNCQPGTS	GVNCEINFDD	CASNPCHG-	ICMDGINRYS	CVCSPGFTGQ	677
RGTCQDPDNA	YLCFCLKGTT	GPNCEINLDD	CASSPCDSG-	TCLDKIDGYE	CACEPGYTGS	673
GGQCTDRENG	YICTCPKGT	GVNCEIKIDD	CASNLCDNG-	KCIDKIDGYE	CTCEPGYTGG	672
DGHCQDRVGS	YYCQCQAGTS	GKNCEVNVNE	CHSNPCNNGA	TCIDGINSYK	CQCVPGFTGQ	710

FIG.13B

hum N	RCNIDIDECA	SNPCRKGATC	INGVNGFRCI	CPEGPHHPSC	YSQVNECLSN	PCI-HGNCCTG
TAN-1	MCNSNIDECA	GNPCHNGGTC	EDGINGFTCR	CPEGYHDPTC	LSEVNECNSN	PCV-HGACRD
Xen N	LCNININECD	SNPCRNGGTC	KDQINGFTCV	CPDGYDHMC	LSEVNECNSN	PCI-HGACHD
Dros N	HCEKNVDECI	SSPCANNGVC	IDQVNGYKCE	CPRGFYDAHC	LSDVDECASN	PCVNEGRCD
hum N	DECASNPCLN	QGTCFDDISG	YTCHCVLPYT	GKNCQTVLAP	CSPNPCENAA	VCKESPNFES
TAN-1	NECASNPCLN	KGTCIDDVAG	YKCNCLLPYT	GATCEVVLAP	CAPSPCRNGG	ECQSEDYES
Xen N	NECSSNPCLN	HGTCIDDVAG	YKCNCLMPYT	GAICEAVLAP	CAGSPCKNGG	RCKESEDFT
Dros N	DDCVTNPCGN	GGTCIDKVNG	YKCVCKVPFT	GRDCESKMDP	CASNRCKNEA	KCTPSSNFLD
hum N	CLANPCQNGG	SCMDGVNTFS	CLCLPGFTGD	KCQTDNMECL	SEPCKNGGTC	SDYVNSYTCK
TAN-1	CRPNPCHNGG	SCTDGINTAF	CDCLPGFRGT	FCEEDINECA	SDPCRNGANC	TDCVDSYTCT
Xen N	CQPNPCHNGG	SCSDGINMFF	CNCPAGFRGP	KCEEDINECA	SNPCKNGANC	TDCVNSYTCT
Dros N	CASFPCQNGG	TCLDGI GDYS	CLCVDGFDGK	HCETDINECL	SQPCQNGATC	SQYVNSYTCT

GLSGYKCLCD	AGWVGINCEV	DKNECLSNPC	QNGGTCNVLV	NGYRCTCKKG	FKGYNCQVNI	796
SLNGYKCDGD	PGWSGTNCDI	NNNECESNPC	VNGGTCKDMT	SGIVCTCREG	FSGPNCQTNI	792
GVNGYKCDCE	AGWSGSNCDI	NNNECESNPC	MNGGTCKDMT	GAYICTCKAG	FSGPNCQTNI	791
GINEFICHCP	PGYTGRCEL	DIDECSSNPC	QHGGTCYDKL	NAFSCQCMGP	YTGQKCE TNI	830
YTCLCA-PCW	QGQRCTIDID	EC-ISKPCMN	HGLCHNTQGS	YMCECPPGFS	GMDCEEDIDD	914
FSCVCPTAGA	KGQTCEVDIN	EC-VLSPCRH	GASQNTHGG	YRCHCQAGYS	GRNCETDIDD	911
FSCECP-PCW	QGQTCEIDMN	EC-VNRPCRN	GATCQNTNGS	YKCNCKPGYT	GRNCEMDIDD	909
FSCTCK-LGY	TGRYCEDID	ECSLSSPCRN	GASCLNVPGS	YRCLCTKGYE	GRDCAINTDD	949
CQAGFDGVHC	ENNINECTES	SCFNNGTCVD	GINSFSC LCP	VGFTGSFCLH	EINECSSHPC	1034
CPAGFSGIHC	ENNTPDCTES	SCFNNGTCVD	GINSFTCLCP	PGFTGSYCQH	VVNECDSRPC	1031
CQPGFSGIHC	ESNTPDCTES	SCFNNGTCID	GINTFTCQCP	PGFTGSYCQH	DINECDSKPC	1029
CPLGFSGINC	QTNDECTES	SCLNGGSCID	GINGYNCSCL	AGYSGANCQY	KLNKCDSNPC	1069

FIG.13C

hum N	LNEGTCVDGL	GTYRCSCPLG	YTGKNCQTLV	NLCSPSPCKN	KGTCVQKKA	EQCLCPSGWA
TAN-1	LLGGTCQDGR	GLHRTCPQG	YTGPNQNLV	HWCDSSPCKN	GGKCWQHTQ	YRCECPSGWT
Xen N	LNGGTCQDSY	GTWKCTCPQG	YTGKNCQNLV	HWCDSSPCKN	GGKCWQTNF	YRCECKSGWT
Dros N	LNGATCHEQN	NEYTCHCPSG	FTGKQCSEYV	DWCGQSPCEN	GATCSQMKHQ	FSCCKSAGWT

hum N	SNPCQHGATC	SDFIGGYRCE	CVPGYQGVNC	EYEVDECQNO	PCQNGGTCID	LVNHFKCSCP
TAN-1	PSPCQNGATC	TDYLGGSCK	CVAGYHGVNC	SEEIDECLSH	PCQNGGTCLD	LPNTYKCS
Xen N	PNPCQNGATC	TDYLGGSCE	CVAGYHGVNC	SEEINECLSH	PCQNGGTCID	LINTYKCS
Dros N	SQPCQNGGTC	RDIGAYECQ	CRQGFQGNQ	ELNIDDCAPN	PCQNGGTCHD	RVMNFS

hum N	CLSNPCSSG	SLDCIQLTND	YLCVCRSAFT	GRHCETFDV	CPQMPCLNGG	TCAVASNM
TAN-1	CLSNPCDARG	TQNCVQRVND	FHCECRAGHT	GRRCESVING	CKGKPCKN	TCAVASNTAR
Xen N	CLSNPCDSRG	TQNCIQLVND	YRCECRQGT	GRRCESVVDG	CKGMPCRNGG	TCAVASNTER
Dros N	CLSNPCSNAG	TLDCVQLVNN	YHCNCRPGHM	GRHCEHKVDF	CAQSPCQNGG	NCNI—RQS

GAYCDVPNV	CDIAASRRGV	LVEHLCQHS	VCINAGNTHY	CQCPLGYTGS	YCEEQLDECA	1154
GLYCDVPSV	CEVAAQRQGV	DVARLCQHGG	LCVDAGNTHH	CRCQAGYTGS	YCEDLVDECS	1151
GVYCDVPSV	CEVAAKQGGV	DIVHLCRNSG	MCVDTGNTHF	CRCQAGYTGS	YCEEQVDECS	1149
GKLCDVQTIS	CQDAADRKGL	SLRQLC—NNG	TCKDYGNSHV	CYCSQGYAGS	YQKEIDECQ	1188

PGTRGLLCEE	NIDDCAR—	—GPHCLN	GGQCMDRIGG	YSCRCLPGFA	GERCEGDINE	1267
RGTQGVHCEI	NVDDCNPPVD	PVSRSPKCFN	NGTCVDQVGG	YSCTCPPGFV	GERCEGDVNE	1271
RGTQGVHCEI	NVDDCTPFYD	SFTLEPKCFN	NGKCIDRVGG	YNCICPPGFV	GERCEGDVNE	1269
PGTMGIICEI	NKDDCKP—	—GACHN	NGSCIDRVGG	FECVCQPGFV	GERCEGDINE	1300

GFICRCPPGF	SGARCQS—	SCGQVKCRKG	EQCVHTAS—	GPRCFCPSP—	—RDCES—	1376
GFICKCPAGF	EGATCENDAR	TCGSLRCLNG	GTICISGPR—	SPTCLCLGPF	TGPECQFPAS	1389
GFICKCPPGF	DGATCEYDSR	TCSNLRQNG	GTICISVLT—	SSKVCSEGY	TGATCQYPVI	1387
GHHICNNGF	YGKNCELSGQ	DCDSNPCRVG	—NCVVADEGF	GYRCECPRG	LGEHCEIDTL	1415

FIG.13D

hum N	-GC-ASSPCQ HGGSCHPQRQ PPIYSCQCAP PFSGRCEL	-YTAPP	-S	TPP
TAN-1	SPCLGGNPCY NQGTCEPTSE SPFYRCLCPA KFNGLLCHIL	DYSFGG	-GAGRD	IPPP
Xen N	SPC-ASHPCY NGGTCQFFAE EPFFQCFCPK NFNGLFCHIL	DYEFPG	-GLGKNIT	TPP
Dros N	DEC-SPNPCA QGAACEDLLG D-YECLCPS KWKGRCDIY	DANYPGWNGG	SGSGNDRYAA	

hum N	NN-QCDELCN TVECLFDNFE CQGNSTCK-	-YDKYCADHF	KDNHCNQGCN	SEECGWDGLD
TAN-1	SDGHCDQCN SAGCLFDGFD CQRAEGQCNP	LYDQYCKDHF	SDGHCDQGCN	SAECEWDGLD
Xen N	NDGKCDQCN NTGCLYDGF DQKVEVQCNP	LYDQYCKDHF	QDGHCDQGCN	NAECEWDGLD
Dros N	KNGKCNNECN NAACHYDGH CERKLKSCDS	LFDAYCQKHY	GDGFCDYGCN	NAECSDWGLD

hum N	YYGEKSAAMK KQ-R		MTRRSL	PGEQ	E	QEVAGSKVFL
TAN-1	YYGREEELRK HPIKRAAEGW AAPDALLGQV	KASLLPGGSE	GRRRRRELDP	MDVRGSIVYL		
Xen N	YYGNEEELKK HHIKRSTDYW SDAPSAI	-FSTMKESIL	LGRHRRELDE	MEVRGSIVYL		
Dros N	WKDNVRVPEI EDTDFARKNK ILYTQQVHQ				-TGIQIYL	

LNR (Notch/Lin-12 Repeats)

---A---TCL	SQYCADKARD	GVCDEACNSH	ACQWDGGDCS	LTMENPWANC	SSPLPCWDYI	1476
LIEE---ACE	LPECQEDAGN	KVCSLQCNH	ACGWDGGDCS	LNFNDPWKNC	TQSLQCWKYF	1501
DNDD---ICE	NEQCSELADN	KVCNANCNNH	ACGWDGGDCS	LNFNDPWKNC	TQSLQCWKYF	1498
DLEQQRAMCD	KRGCTEKQGN	GICSDSCNTY	ACNFDGNDCS	LGI-NPWANC	TAN-EXWNKF	1531

CAADQPEN-L	AEGTLVIVVL	MPPEQLLQDA	R-SFLRALGT	LLHTNLRIKR	DSQGELMVYP	1591
CAEHVPER-L	AAGTL-VVVV	LMPPEQLRNS	SFHLRELSR	VLHTNVVFKR	DAHQQMIFP	1619
C-ANMPEN-L	AEGTLVLVVL	MPPERLKNNS	V-NFLRELSR	VLHTNVVFKK	DSKGEYKIYP	1615
CENKTQSPVL	AEGAMSVVML	MNVEAFREIQ	A-QFLRNMSH	MLRTTVRLKK	DALGHDIIN	1650

EIDNRQCVDQ	SDHCFKNTDA	AAALLASHAI	QG---TLYP	LVSVVSESLT	PERT-Q	LY	1680
EIDNRQCQVA	SSQCFQSATD	VAAFLGALAS	LGSL-NIPYK	IEAVQSETVE	PPPPAQ	LHF	1737
EIDNRQCQYS	SSQCFNSATD	VAAFLGALAS	LGSLDTLSYK	IEAVKSENME	TPKPST	LYP	1730
EIDNRKCTEC	FTHAVEAAEF	LAATAAKHQL	RNDFQ-IHSV	RGIKNPGDED	NGEPPANV	KY	1745

FIG.13E

hum N	LLAVAVVIL FIILLGVIMA	KRKRK--HGS LWLPEGFTLR RDASNHKRRE	PVGQDAVGLK
TAN-1	MYVAAAFVL LFFVGCGVL	SRKRRRQHGQ LWFPEGFKV- SEASKKKRRE	ELGEDSVGLK
Xen N	MLSMLVIPLL IIFVFMVIV	NKKRRREHDS FGSPTALFQK NPA-KRNGET	PW-EDSVGLK
Dros N	VITGIILVII ALAFFGMVL	STQRKRAHGV TWPEGFRAP AAVMSRRRRD	PHGQEMRNLN

CDC-10/Ankyrin Repeats

hum N	PIDRRPWTQQ HLEAADIRRT	PSLALTPPQA EQEVDVLDVN VRGPDGCTPL	MLASLRGGSS
TAN-1	QTDHRQWTQQ HLDAADL-RM	SAMAPTPPQG EVDADCMDVN VRGPDGFTPL	MIASCSGGGL
Xen N	KTDPRQWTRQ HLDAADL-RI	SSMAPTPPQG EIEADCMDVN VRGPDGFTPL	MIASCSGGGL
Dros N	EADQRVWSQA HLDVVDV-R-	AIM--TPP-A HQDGGKHVDV	ARGPCGLTPL MIAAVRGGGL

hum N	ANAQDNMGRG PLHAAVAADA	QGVFQILIRN RVTOLDARMN DGTPLILAA	RLAVEGMVAE
TAN-1	ANIQDNMGRG PLHAASADA	QGVFQILIRN RATOLDARMH DGTPLILAA	RLAVEGMLED
Xen N	ANVQDNMGRG PLHAAVAADA	QGVFQILIRN RATOLDARMF DGTPLILAA	RLAVEGMVEE
Dros N	ANCQDNTGRG PLHAAVAADA	MGVFQILLRN RATNLNARMH DGTPLILAA	RLATEGMVED

NLSVQVSEAN LIGTGTSEHW VDDE	-----G	PQPKKVAED EALLSE-EDD	1782
PLK-NASDGA LMDNQNE-W GDED	-----	LETKKRFEE PVVLPD-LDD	1837
PIK-NMTDGS FMDNQNE-W GDEET	-----	LENKRFRFEE QVILPELVDD	1831
KQVAMQSQGV QPGAH--W SDESMDPLP	KRQRSDPVSG	VGLGNNGGYA SDHTMVSEYE	1861

DLSEDEDAE DSSANIITDL VYQGASLQAO	TDRTGEMALH LAARYSRADA	AKRLLDAGAD	1902
ETGNSEEE-E DAPA-VISDF IYQGASLHNQ	TDRTGETALH LAARYSRSDA	AKRLLASAD	1954
ETGNSEEE-E DASANMISDF ICQGAQLHNQ	TDRTGETALH LAARYARADA	AKRLLSSAD	1949
LTGEDIENTNE DSTAQVISDL LAQGAELNAT	MDKTGETSLH LAARFARADA	AKRLLDAGAD	1976

LINCQADVNA VDDHGKSALH WAAAVNNVEA	TLLLLKNGAN RDMQDNKEET	PLFLAAREGS	2022
LINSHADVNA VDDLCKSALH WAAAVNNVDA	AVVLLKNGAN KDMQNNREET	PLFLAAREGS	2074
LINAHADVNA VDEFGKSALH WAAAVNNVDA	AAVLLKNSAN KDMQNNKEET	SLFLAAREGS	2069
LITADADINA ADNSGKTALH WAAAVNNTEA	VNILLMHAN RDAQDDKDET	PLFLAAREGS	2096

FIG.13F





hum N	GSAGLSRLH	PVPVPADW--	MNRMEVNETQ	YNEMFGMVL	PAEG-THPGI	APQSRPPECK
TAN-1	GQCEWLSRLQ	SGMVPNQYNP	LRGSAVPGPL	STQAPSLQHG	-MVGPLHSSL	AASALSQMMS
Xen N	SQCDWLARLQ	NGMVQNQYDP	IRNGIQQGN-	AQQAQALQHG	LMTS-LHNGL	PATTLQMMT
Dros N	PSLPTSPTHI	QAMRHATQK	QFGGSLNSL	LGGANGGGV	GGGGGGGGV	GQGPQNSPVS

hum N	APQPSTCPP	AVAGPLPTMY	QIP-----	EM ARL-PSVAF	TAMPQQDQ	VAQTILPAYH
TAN-1	PPQPHLGVS	AASGHLGRSF	LSGEPQADV	QPLGPSSLAV	HTILPQ-ESP	ALPTSLPSSL
Xen N	MQQHHN-SS	TTSTHINSF	CSSDISQDL	QQM-SSNNI	HSVMPQ-DTQ	IFAASLPN
Dros N	QQQLGLEFG	SAGLDLNG-F	CGSPDSFHSG	QMNPPS---	I QSSMSG-SSP	STNMLSPSSQ

hum N	SDWSDVTSP	TPGGAGGQR	GPGTHMSEPPHN	MQVYA
TAN-1	SDWSEGVSSP	PT-----	SMQ SQIARIP	EAFAK
Xen N	SDWSEGISSP	PT-----	SMQ PQRTHIP	EAFAK
Dros N	SDWSEGVQSP	AANNLYISGG	HQANKGSEAIYI	

-----	-----	HITTPRE	PLPP-IV-TF	QLIPKGSIAQ	PAG-----	2320
-----	-----	-YQGLPSTR	ATQPHLVQTQ	QVQPQNLQMQ	QQLQPANIQ	QQQSLQPPPP 2414
-----	-----	-YQAMPNTR	ANQPHLMQAQ	QMQQQQN---	-----	LQLHQS 2384
LGIIPTGSD	MGIMLAPPQS	SKNSAIMQTI	SPQQQQQQQQ	QQQQQHQQQQ	QQQQQQQQQQ	2565

PEST -containing Region

PFPASVGKYP	TPPSQHSYAS	SNAARTPSH	SGHLQGEHPY	LTPSPESPQ	WSSSSPHSA-	2433
VPPVTAAQFL	TPPSQHSY-S	S-PVENTPSH	QLQVP-EGPF	LTPSPESPQ	WSSSSPHSNV	2530
TQSMTTAQFL	TPPSQHSY-S	S-PMDNTPSH	QLQVP-DHPF	LTPSPESPQ	WSSSSPHSNM	2497
HNQQAQFYQL	TPSSQHS---	CGHTPQH	LVQTL-D-SY	PTSPESPQH	WSSSSPRSN-	2671

2471  
2556  
2523  
2703

FIG.13H

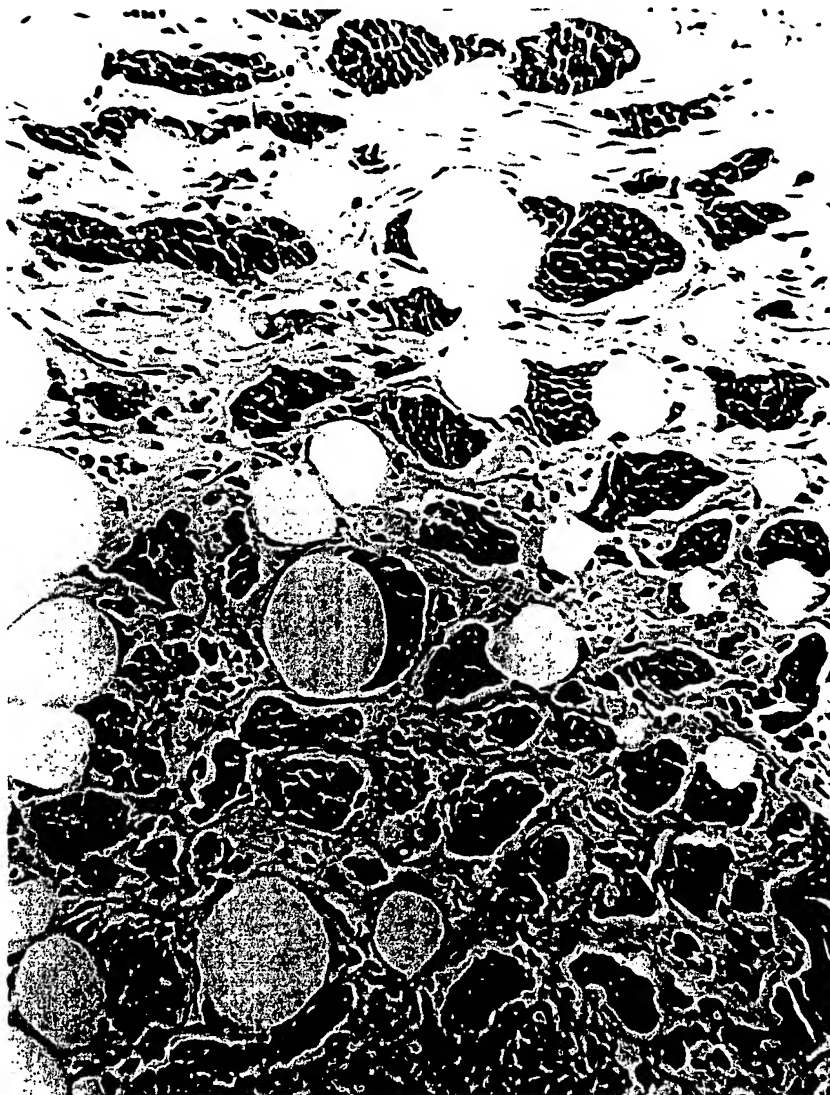


FIG.14



FIG.15A



FIG.15B



FIG.16A

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Serial No.: 10/781,060

Inventor(s): Artavanis-Tsakonas et al.

Title: Therapeutic and Diagnostic Methods and  
Compositions Based on Notch Proteins and Nucleic Acids



FIG. 16B

```

      10      20      30      40      50      60      70      80      90
      *      *      *      *      *      *      *      *      *
GGAATCCGC CCGCCCTGC CCCCCTCTC CTGTGGGGC TGCTGGCGCT CTGGCTGTGC TCGCGGGCC CCGCGCATGC ATTGCAGTGT
      P A L R P A L L W A L L A L W L C C A A P A H A L Q >

     100     110     120     130     140     150     160     170     180
     *      *      *      *      *      *      *      *      *
CGAGATGGCT ATGAACCTG TGTAAATGAA GGAATGTGT TTACCTACCA CAATGGCACA GGATACTGCA AATGTCCAGA AGGCTTCTTG
      R D G Y E P C V N E G M C V T Y H N G T G Y C K C P E G F L>

     190     200     210     220     230     240     250     260     270
     *      *      *      *      *      *      *      *      *
GGGAATATT GTCAACATCG AGACCCCTGT GAGAAGAACC GCTGCCAGAA TGGTGGGACT TGTGTGGCCC AGGCCATGCT GGGGAAAGCC
      G E Y C Q H R D P C E K N R C Q N G G T C V A Q A M L G K A>

     280     290     300     310     320     330     340     350     360
     *      *      *      *      *      *      *      *      *
ACGTGCCGAT GTGCCTCAGG GTTACAGGA GAGGACTGCC AGTACTCAAC ATCTCATCCA TGCTTTGTGT CTCGACCTCG CCTGAATGGC
      T C R C A S G F T G E D C Q Y S T S H P C F V S R P C L N G>

     370     380     390     400     410     420     430     440     450
     *      *      *      *      *      *      *      *      *
GGCAGATGCC ATATGCTCAG CCGGGATACC TATGAGTGCA CCTGTCAAGT CCGGTTTACA GGTAAGGACT GCCAATGGAC GGATGCCTGC
      G T C H M L S R D T Y E C T C Q V G F T G K E C Q W T D A C>

     460     470     480     490     500     510     520     530     540
     *      *      *      *      *      *      *      *      *
CTGTCTCATC CCTGTGAAA TGAAGTACC TGTACCACTG TGGCCAACCA GTTCTCCTGC AAATGCCTCA CAGGCTTCAC AGGGCAGAAA
      L S H P C A N G S T C T T V A N Q F S C K C L T G F T G Q K>

     550     560     570     580     590     600     610     620     630
     *      *      *      *      *      *      *      *      *
TGTGAGACTG ATGTCAATGA GTGTGACATT CCAGGACACT GCCAGCATGG TGGCACCTGC CTCAACCTGC CTGTTCTCTA CCAGTGCCAG
      C E T D V N E C D I P G H C Q H G G T C L N L P G S Y Q C Q>

     640     650     660     670     680     690     700     710     720
     *      *      *      *      *      *      *      *      *
TGGCCTCAGG GCTTCACAGG CCAGTACTGT GACAGCCTGT ATGTGCCCTG TGCACCTCA CCTTGTGTCA ATGGAGGCAC CTGTGGGCAG
      C P Q G F T G Q Y C D S L Y V P C A P S P C V N G G T C R Q>

     730     740     750     760     770     780     790     800     810
     *      *      *      *      *      *      *      *      *
ACTGGTGACT TCACITTTGA GTGCAACTGC CTCCAGGT TTGAAGGGAG CACCTGTGAG AGGAATATTG ATGACTGCCC TAACCACAGG
      T G D F T F E C N C L P G F E C S T C E R N I D D C P N H R>

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FIG.17A



820 830 840 850 860 870 880 890 900  
\* \* \* \* \*  
TGTCAGAATC GAGGGGTTTG TGTGGATGGG GTCAACACTT ACAACTGCCG CTGTCCCCCA CAATGGACAG GACAGTTCTG CACAGAGGAT  
C Q N G G V C V D G V N T Y N C R C P P Q W T G Q F C T E D>

910 920 930 940 950 960 970 980 990  
\* \* \* \* \*  
GTGGATGAAT GCCTGCTGCA GCCCAATGCC TGTCAAAATG GGGGCACCTG TGCCAACCCG AATGGAGGCT ATGGCTGTGT ATGTGTCAAC  
V D E C L L Q P N A C Q N G G T C A N R N G G Y G C V C V N>

1000 1010 1020 1030 1040 1050 1060 1070 1080  
\* \* \* \* \*  
GGCTGGAGTG GAGATCACTG CACTGAGAAC ATTGATGATT GTGCCTTCCG CTCCTGTACT CCAGGCTCCA CCTGCATCGA CCGTGTGGCC  
G W S G D D C S E N I D D C A F A S C T P G S T C I D R V A>

1090 1100 1110 1120 1130 1140 1150 1160 1170  
\* \* \* \* \*  
TCCTTCTCTT GCATGTGCCC AGAGGGGAAG GCAGGTCTCC TGTGTCTATCT GGATGATGCA TGCATCAGCA ATCCTTGCCA CAAGGGGGCA  
S F S C M C P E G K A G L L C H L D D A C I S N P C H K G A>

1180 1190 1200 1210 1220 1230 1240 1250 1260  
\* \* \* \* \*  
CTGTGTGACA CCAACCCCTT AAATGGGCAA TATATTTGCA CCTGCCCACA AGGCTACAAA GGGGCTGACT GCACAGAAGA TGTGGATGAA  
L C D T N P L N G Q Y I C T C P Q G Y K G A D C T E D V D E>

1270 1280 1290 1300 1310 1320 1330 1340 1350  
\* \* \* \* \*  
TGTGCCATGG CCAATAGCAA TCCTTGTGAG CATGCAGGAA AATGTGTGAA CACGGATGGC GCCTTCCACT GTGAGTGTCT GAAGGGTTAT  
C A M A N S N P C E H A G K C V N T D G A F H C E C L K G Y>

1360 1370 1380 1390 1400 1410 1420 1430 1440  
\* \* \* \* \*  
GCAGGACCTC GTTGTGAGAT GGACATCAAT GAGTGCCATT CAGACCCCTG CCAGAATGAT GCTACCTGTC TCGATAAGAT TGGAGGCTTC  
A G P R C E M D I N E C H S D P C Q N D A T C L D K I G G F>

1450 1460 1470 1480 1490 1500 1510 1520 1530  
\* \* \* \* \*  
ACATGTCTGT GCATGCCAGG TTTCAAAGGT GTCCATTGTG AATTAGAAAT AAATGAATGT CAGACCAACC CITGTGTGAA CAATGGGCAG  
T C L C M P G F K G V H C E L E I N E C Q S N P C V N N G Q>

1540 1550 1560 1570 1580 1590 1600 1610 1620  
\* \* \* \* \*  
TGTGTGGATA AAGTCAATCG TTTCCAGTGC CTGTGTCCTC CTGGTTTCAC TGGGCCAGTT TGCCAGATTG ATATTGATGA CTGTTCCAGT  
C V D K V N R F Q C L C P P G F T G P V C Q I D I D D C S S>

FIG.17B

1630	1640	1650	1660	1670	1680	1690	1700	1710
ACTCCGTGTC	TGAATGGGG	AAAGTGTATC	GATCACCGCA	ATGGCTATGA	ATGCCAGTGT	GGCACAGGTT	TCACTGGTGT	GTGTGTGAG
T P C	L N G A	K C I	D H P	N G Y E	C Q C	A T G	F T G V	L C E>
1720	1730	1740	1750	1760	1770	1780	1790	1800
GAGAACATTG	ACAACTGTGA	CCCCGATCCT	TGCCACCATG	GTCAGTGTCA	GGATGGTATT	GATTCCTACA	CCTGCATCTG	CAATCCCGGG
E N I	D N C D	P D P	C H H	G Q C Q	D G I	D S Y	T C I C	N P G>
1810	1820	1830	1840	1850	1860	1870	1880	1890
TACATGGGGC	CCATCTGCAG	TGACCAGATT	GATGAATGTT	ACAGCAGCCC	TTGCCTGAAC	GATGGTCGCT	GCATTGACCT	GGTCAATGGC
Y M G	A I C S	D Q I	D E C	Y S S P	C L N	D G R	C I D L	V N G>
1900	1910	1920	1930	1940	1950	1960	1970	1980
TACCACTGCA	ACTGCCAGCC	AGGCCAGTCA	GGGTTAATT	GTGAAATTAA	TTTTGATCAC	TGTGCAAGTA	ACCCTGTAT	CCATGGAATC
Y Q C	N C Q P	G T S	G V N	C E I N	F D D	C A S	N P C I	H G I>
1990	2000	2010	2020	2030	2040	2050	2060	2070
TGTATCGATG	GCATTAATCG	CTACAGTTGT	GTCGCTCAC	CAGGATTCAC	AGGCCAGAGA	TGTAACATTG	ACATTGATGA	GTGTGCCTCC
C M D	G I N R	Y S C	V C S	P G F T	G Q R	C N I	D I D E	C A S>
2080	2090	2100	2110	2120	2130	2140	2150	2160
AATCCCTGTC	GCAAGGTGTC	AACATGTATC	AACGGTGTGA	ATGGTTTCCG	CTGTATATGC	CCCGAGGGAC	CCCATACCCC	CAGCTGCTAC
N P C	R K G A	T C I	N G V	N G F R	C I C	P E G	P H H P	S C Y>
2170	2180	2190	2200	2210	2220	2230	2240	2250
TCACAGGTGA	ACGAATGCCT	GAGCAATCCC	TGCATCCATG	GAAACTGTAC	TGGAGGTCTC	AGTGGATATA	AGTGTCTCTG	TGATGCAGGC
S Q V	N E C L	S N P	C I H	G N C T	G G L	S G Y	K C L C	D A G>
2260	2270	2280	2290	2300	2310	2320	2330	2340
TGGGTTGCCA	TCAACTGTGA	ACTGGACAAA	AATGAATGCC	TTTCCAATCC	ATGCCAGAAT	GGAGGAACIT	GTGACAATCT	GGTGAATGGA
W V G	I N C E	V D K	N E C	L S N P	C Q N	G G T	C D N L	V N G>
2350	2360	2370	2380	2390	2400	2410	2420	2430
TACAGGTGTA	CTTCCAAGAA	GGCCTTTAAA	GGCTATAACT	CCCAGGTGAA	TATTGATGAA	TGTGCCTCAA	ATCCATGCCT	GAACCAAGGA
Y R C	T C K F	G F K	G Y N	C Q V N	I D E	C A S	N P C L	N Q G>

FIG.17C

2440	2450	2460	2470	2480	2490	2500	2510	2520
ACCTGCTTTG	ATGACATAAG	TGGCTACACT	TGCCACTGTG	TGCTGCCATA	CACAGGCAAG	AATTGTCAGA	CAGTATTGGC	TCCTGTITCC
T C F D D I S	G Y T C H C	V L P Y T G K	N C Q T V L A	P C S>				
2530	2540	2550	2560	2570	2580	2590	2600	2610
CCAAACCCCT	GTGAGAATGC	TGCTGTTTGC	AAAGAGTCAC	CAAATTTTGA	CAGTTATACT	TGCTTGTGTG	CTCCTGGCTG	GCAAGGTCAG
P N P C E N A	A V C K E S	P N F E S Y T	C L C A P G W	Q G Q>				
2620	2630	2640	2650	2660	2670	2680	2690	2700
CGGTGTACCA	TTGACATTGA	CGAGTGTATC	TCCAAGCCCT	GCATGAACCA	TGGTCTCTGC	CATAACACCC	AGGGCAGCTA	CATGTGTGAA
R C T I D I D	E C I S K P	C M N H G L C	H N T Q G S Y	M C E>				
2710	2720	2730	2740	2750	2760	2770	2780	2790
TGTCCACCAG	GCTTCAGTGG	TATGGACTGT	GAGGAGGACA	TTGATGACTG	CCTTGCCAAT	CCTTGCCAGA	ATGGAGGTTT	CTGTATGGAT
C P P G F S G	M D C E E D	I D D C L A N	P C Q N G G S	C M D>				
2800	2810	2820	2830	2840	2850	2860	2870	2880
GGAGTGAATA	CTTTCTCCTG	CCTCTGCCIT	CCGGGTTTCA	CTGGGGATAA	GTGCCAGACA	GACATGAATG	AGTGTCTGAG	TGAACCCCTGT
G V N T F S C	L C L P G F	T G D K C Q T	D M N E C L S	E P C>				
2890	2900	2910	2920	2930	2940	2950	2960	2970
AAGAATGGAG	GGACCTGCTC	TGACTACGTC	AACAGTTACA	CTTGCAAGTG	CCAGGCAGGA	TTTGATGGAG	TCCATTGTGA	GAACAACATC
K N G G T C S	D Y V N S Y	T C K C Q A G	F D G V H C E	N N I>				
2980	2990	3000	3010	3020	3030	3040	3050	3060
AATCAGTGCA	CTGAGAGCTC	CTGTTTCAAT	GGTGGCACAT	GTGTGATGCG	GATTAACCTCC	TTCTCTTGCT	TGTGCCCTGT	GGGTTTCACT
N E C T E S S	C F N G G T	C V D G I N S	F S C L C P V	G F T>				
3070	3080	3090	3100	3110	3120	3130	3140	3150
GGATCCTTCT	GCCTCCATGA	GATCAATGAA	TGCAGCTCTC	ATCCATGCCT	GAATGAGGGA	ACGTGTGTTG	ATGGCCTGGG	TACCTACCCG
G S F C L H E	I N E C S S	H P C L N E G	T C V D G L G	T Y R>				
3160	3170	3180	3190	3200	3210	3220	3230	3240
TGCAGCTGCC	CCCTGGGCTA	CACTGGGAAA	AAGTGTGAGA	CCCTGGTGAA	TCTCTGCAGT	CGGTCTCCAT	GTA AAAACAA	AGGTACTTGT
C S C P L G Y	T G K N C Q	T L V N L C S	R S P C K N K	G T C>				

```

3250      3260      3270      3280      3290      3300      3310      3320      3330
*         *         *         *         *         *         *         *         *
GITCAGAAAA AAGCAGAGTC CCAGTGCCTA TGTCCATCTG GATGGGCTGG TGCCTATTGT GACGTGCCCC ATGCTCTCTG TGACATAGCA
V Q K K A E S Q C L C P S G W A G A Y C D V P N V S C D I A>

3340      3350      3360      3370      3380      3390      3400      3410      3420
*         *         *         *         *         *         *         *         *
GCCTCCAGGA GAGGTGTGCT TGTGAACAC TTGTGCCAGC ACTCAGGTGT CTGCATCAAT GCTGCCAACA CGCATTACTG TCAGTGCACC
A S R R G V L V E H L C Q H S G V C I N A G N T H Y C Q C P>

3430      3440      3450      3460      3470      3480      3490      3500      3510
*         *         *         *         *         *         *         *         *
CTGGGCTATA CTGGGAGCTA CTGTGAGGAG CAACTCGATG AGTGTGGCTC CAACCCCTGC CAGCACGGGG CAACATGCAG TGACTTCATT
L G Y T G S Y C E E Q L D E C A S N P C Q H G A T C S D F I>

3520      3530      3540      3550      3560      3570      3580      3590      3600
*         *         *         *         *         *         *         *         *
GGTGGATACA GATGCCAGTG TGTCCCAGGC TATCAGCGTG TCAACTGTGA GTATGAAGTG GATGAGTGCC AGAATCAGCC CTGCCAGAAT
G G Y R C E C V P G Y Q G V N C E Y E V D E C Q N Q P C Q N>

3610      3620      3630      3640      3650      3660      3670      3680      3690
*         *         *         *         *         *         *         *         *
GGAGGCACCT GTATTGACCT TGTGAACCAT TTCAAGTGCT CTTGCCCAAC AGGCACTCGG GGCCTACTCT GTGAAGAGAA CATTGATGAC
G G T C I D L V N H F K C S C P P G T R G L L C E E N I D D>

3700      3710      3720      3730      3740      3750      3760      3770      3780
*         *         *         *         *         *         *         *         *
TGTGCCCGGG GTCCCCATTG CCTTAATGCT GGTCACTGCA TGGATAGGAT TGGAGGCTAC AGTGTGCGCT GCTTGCCCTG CTTTGCTGGG
C A R G P H C L N G G Q C M D R I G G Y S C R C L P G F A G>

3790      3800      3810      3820      3830      3840      3850      3860      3870
*         *         *         *         *         *         *         *         *
GAGCGTGTG AGGGAGACAT CAACGAGTGC CTCTCCAACC CCTGCAGCTC TGAGGGCAGC CTGGAAGTGA TACAGCTCAC CAATGACTAC
E R C E G D I N E C L S N P C S S E G S L D C I Q L T N D Y>

3880      3890      3900      3910      3920      3930      3940      3950      3960
*         *         *         *         *         *         *         *         *
CTGTGTGTTT GCCGTAGTGC CTTTACTGGC CGGCACTGTG AAACCTTCGT CGATGTGTGT CCCCAGATGC CCTGCCTGAA TGGAGGGACT
L C V C R S A F T G R H C E T F V D V C P Q M P C L N G G T>

3970      3980      3990      4000      4010      4020      4030      4040      4050
*         *         *         *         *         *         *         *         *
TGTGCTGTGG CCAGTAACAT GCCTGATGCT TTCATTGCC GTTGTCCTCC GGGATTTTCC GGGGCAAGGT GCCAGAGCAG CTGTGGACAA
C A V A S N M P D G F I C R C P P G F S G A R C Q S S C G Q>

```

FIG 17F

4060 4070 4080 4090 4100 4110 4120 4130 4140  
\* \* \* \* \*  
GTGAAATGTA GGAAGGCGGA GCAGTGTGTG CACACCCCT CTGGACCCCG CTGCTTCTGC CCCAGTCCCC GGGACTGCCA GTCAGGCTGT  
V K C R K G E Q C V H T A S G P R C F C P S P R D C E S G C>

4150 4160 4170 4180 4190 4200 4210 4220 4230  
\* \* \* \* \*  
GCCAGTAGCC CCTGCCAGCA CCGGGGCAGC TGCCACCCCTC AGCGCCAGCC TCCTTATTAC TCCTGCCAGT GTGCCCCACC ATTCTCGGCT  
A S S P C Q H G G S C H P Q R Q P P Y Y S C Q C A P P F S G>

4240 4250 4260 4270 4280 4290 4300 4310 4320  
\* \* \* \* \*  
AGCCGCTGTG AACTCTACAC GGCACCCCCC AGCACCCCTC CTGCCACCTG TCTGAGCCAG TATTGTGCCG ACAAAGCTCG GGATGGCGTC  
S R C E L Y T A P P S T P P A T C L S Q Y C A D K A R D G V>

4330 4340 4350 4360 4370 4380 4390 4400 4410  
\* \* \* \* \*  
TGTGATGAGC CCTGCAACAG CCATGCCTGC CAGTGGGATG GGGGTGACTG TTCTCTCACC ATGGAAGAACC CCTGGGCCAA CTGCTCCTCC  
C D E A C N S H A C Q W D G G D C S L T M E N P W A N C S S>

4420 4430 4440 4450 4460 4470 4480 4490 4500  
\* \* \* \* \*  
CCACTTCCTT GCTGGGATTA TATCAACAAC CAGTGTGATG AGCTGTGCAA CACGGTCCAG TGCTGTGTTG ACAACTTTGA ATGCCAGGGC  
P L P C W D Y I N N Q C D E L C N T V E C L F D N F E C Q G>

4510 4520 4530 4540 4550 4560 4570 4580 4590  
\* \* \* \* \*  
AACAGCAAGA CATGCAAGTA TGACAAATAC TGTGCAGACC ACTTCAAAGA CAACCACTGT AACCAGGGGT GCAACAGTGA GGAGTGTGCT  
N S K T C K Y D K Y C A D H F K D N H C N Q G C N S E E C G>

4600 4610 4620 4630 4640 4650 4660 4670 4680  
\* \* \* \* \*  
TGGGATGGCC TGGACTGTGC TGCTGACCAA CCTGAGAACC TGGCAGAAGG TACCTGGTT ATTGTGGTAT TGATGCCACC TGAACAACCT  
W D G L D C A A D Q P E N L A E G T L V I V V L M P P E Q L>

4690 4700 4710 4720 4730 4740 4750 4760 4770  
\* \* \* \* \*  
CTCCAGGATG CTGCAGCTT CTGCGGGCA CTGGGTACCC TGCTCCACAC CAACCTGCCC ATTAAGCGCG ACTCCAGGG GGAACCTCATG  
L Q D A R S F L R A L G T L L H T N L R I K R D S Q G E L M>

4780 4790 4800 4810 4820 4830 4840 4850 4860  
\* \* \* \* \*  
GTGTACCCCT ATTATGGTGA GAAGTCAGCT GCTATGAAGA AACAGAGGAT GACACGCAGA TCCCTTCCTG GTGAACAAGA ACAGGAGGTC  
V Y P Y Y G E K S A A M K K Q R M T R R S L P G E Q E Q E V>

FIG.17F

4870 4880 4890 4900 4910 4920 4930 4940 4950  
\* \* \* \* \*  
GCTGGCTCTA AAGTCTTTCT CGAAATTGAC AACCGCCAGT GTGTCAAGA CTCAGACCAC TGCTTCAAGA ACACGGATGC AGCAGCAGCT  
A G S K V F L E I D N R Q C V Q D S D H C F K N T D A A A A>  
4960 4970 4980 4990 5000 5010 5020 5030 5040  
\* \* \* \* \*  
CTCCTGGCCT CTCACGCCAT ACAGGGGACC CTGTCATACC CTCTTGTC TCCTCTCAGT GAATCCCTGA CTCAGAACC CACTCAGCTC  
L L A S H A I Q G T L S Y P L V S V V S E S L T P E R T Q L>  
5050 5060 5070 5080 5090 5100 5110 5120 5130  
\* \* \* \* \*  
CTCTATCTCC TTGCTGTGCG TGTGTCATC ATTCTGTTA TTATTCTGCT GGGCGTAATC ATGGCAAAAC GAAAGCGTAA GCATGGCTCT  
L Y L L A V A V V I I L F I I L L G V I M A K R K R K H G S>  
5140 5150 5160 5170 5180 5190 5200 5210 5220  
\* \* \* \* \*  
CTCTGGCTGC CTGAAGGTTT CACTCTTCGC CGAGATGCAA GCAATCACA GCGTCGTGAG CCAGTGGGAC AGGATGCTGT GGGCGTGAAA  
L W L P E G F T L R R D A S N H K R R E P V G Q D A V G L K>  
5230 5240 5250 5260 5270 5280 5290 5300 5310  
\* \* \* \* \*  
AATCTCTCAG TGCAAGTCTC AGAAGCTAAC CTAATTGGTA CTGGAACAAG TGAACACTGG GTCGATGATG AAGGGCCCCA GCCAAAGAAA  
N L S V Q V S E A N L I G T G T S E H W V D D E G P Q P K K>  
5320 5330 5340 5350 5360 5370 5380 5390 5400  
\* \* \* \* \*  
GTAAAGGCTG AAGATGAGGC CTTACTCTCA GAAGAAGATG ACCCCATTGA TCGACGGCCA TGGACACAGC AGCACCTTGA AGCTGCAGAC  
V K A E D E A L L S E E D D P I D R R P W T Q Q H L E A A D>  
5410 5420 5430 5440 5450 5460 5470 5480 5490  
\* \* \* \* \*  
ATCCGTAGGA CACCATGCGT GGCTCTCACC CCTCCTCAGC CAGAGCAGGA GGTGATGTG TTAGATGTGA ATGTCCGTGG CCCAGATGGC  
I R R T P S L A L T P P Q A E Q E V D V L D V N V R G P D G>  
5500 5510 5520 5530 5540 5550 5560 5570 5580  
\* \* \* \* \*  
TGCACCCCAT TGATGTGGC TTCTCTCCGA CGAGGCAGCT CAGATTGAG TGATGAAGAT GAAGATGCAG AGGACTCTTC TGCTAACATC  
C T P L M L A S L R G G S S D L S D E D E D A E D S S A N I>  
5590 5600 5610 5620 5630 5640 5650 5660 5670  
\* \* \* \* \*  
ATCAGAGACT TGGTCTACCA GGGTCCAGC CTCCAGGCCC AGACAGACCG GACTGGTGAG ATGGCCCTGC ACCTTGCAGC CCGCTACTCA  
I T D L V Y Q G A S L Q A Q T D R T G E M A L H L A A R Y S>

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    6490      6500      6510      6520      6530      6540      6550      6560      6570
    *        *        *        *        *        *        *        *        *
ACGTATGTTT CCGACACCAC ATCCTCTCCA ATGATTACAT CCCCTGGGAT CTTACAGGCC TCACCCAACC CTATGTTGGC CACTGCCGCC
T Y V S D T T S S P M I T S P G I L Q A S P N P M L A T A A>

    6580      6590      6600      6610      6620      6630      6640      6650      6660
    *        *        *        *        *        *        *        *        *
CCTCCTGCCC CAGTCCATGC CCAGCATGCA CTATCTTTT CTAACCTTCA TGAATGCCAG CCTTTGGCAC ATGGGGCCAG CACTGTGCTT
P P A P V H A Q H A L S F S N L H E M Q P L A H G A S T V L>

    6670      6680      6690      6700      6710      6720      6730      6740      6750
    *        *        *        *        *        *        *        *        *
CCCTCAGTGA GCCAGTIGCT ATCCACCCAC CACATTGTGT CTCCAGGCAG TGGCAGTGCT GGAAGCTTGA GTAGGCTCCA TCCAGTCCCA
P S V S Q L L S H H H I V S P G S G S A G S L S R L H P V P>

    6760      6770      6780      6790      6800      6810      6820      6830      6840
    *        *        *        *        *        *        *        *        *
GTCCACGAGC ATTGGATGAA CCGCATGGAG GTGAATGAGA CCCAGTACAA TGAGATGTTT GGTATGGTCC TGGCTCCAGC TGAGGCGACC
V P A D W M N R M E V N E T Q Y N E M F G M V L A P A E G T>

    6850      6860      6870      6880      6890      6900      6910      6920      6930
    *        *        *        *        *        *        *        *        *
CATCCTGGCA TAGCTCCCCA GAGCAGGCCA CCTGAAGGGA AGCACATAAC CACCCCTCGG GAGCCCTTGC CCCCATTGT GACTTTCAG
H P G I A P Q S R P P E G K H I T T P R E P L P P I V T F Q>

    6940      6950      6960      6970      6980      6990      7000      7010      7020
    *        *        *        *        *        *        *        *        *
CTCATCCCTA AAGGCAGTAT TGCCCAACCA GCGGGGGCTC CCCAGCCTCA GTCCACCTGC CCTCCAGCTG TTGCGGGCCC CCTGCCACCC
L I P K G S I A Q P A G A P Q P Q S T C P P A V A G P L P T>

    7030      7040      7050      7060      7070      7080      7090      7100      7110
    *        *        *        *        *        *        *        *        *
ATGTACCAGA TTCCAGAAAT GGGCCGTTTG CCCAGTGTGG CTTTCCCCAC TGCCATGATG CCCCAGCAGG ACGGGCAGGT AGCTCAGACC
M Y Q I P E M A R L P S V A F P T A M M P Q Q D G Q V A Q T>

    7120      7130      7140      7150      7160      7170      7180      7190      7200
    *        *        *        *        *        *        *        *        *
ATTCTCCCAG CCTATCATCC TTTCCAGCC TCTGTGGGCA AGTACCCAC ACCCCCTTCA CAGCACAGTT ATGCTTCCTC AAATGCTGCT
I L P A Y H P F P A S V G K Y P T P P S Q H S Y A S S N A A>

    7210      7220      7230      7240      7250      7260      7270      7280      7290
    *        *        *        *        *        *        *        *        *
GAGCGAACAC CCAGTCACAG TGGTCACCTC CAGGGTGAGC ATCCCTACCT GACACCATCC CCAGAGTCTC CTGACCAGTG GTCAAGTTCA
E R T P S H S G H L Q G E H P Y L T P S P E S P D Q W S S S>
  
```

FIG.171

7300	7310	7320	7330	7340	7350	7360	7370	7380
*	*	*	*	*	*	*	*	*
TCACCCCACT	CTGCTTCTGA	CTGGTCAGAT	GTGACCACCA	GGCCTACCCC	TGGGGGTGCT	GGAGGAGGTC	AGCGGGGACC	TGGGACACAC
S P H	S A S D	W S D	V T T	S P T P	G G A	G G G	Q R G P	G T H>

7390	7400	7410	7420	7430	7440	7450	7460	7470
*	*	*	*	*	*	*	*	*
ATGTCTGAGC	CACCACACAA	CAACATGCAG	GTTTATGCGT	GAGAGAGTCC	ACCTCCAGTG	TAGAGACATA	ACTGACTTTT	GTAAATGCTG
M S E	P P H N	N M Q	V Y A>					

7480	7490	7500	7510	7520	7530	7540	7550	7560
*	*	*	*	*	*	*	*	*
CTGAGGAACA	AATGAAGGTC	ATCCGGGAGA	GAAATGAAGA	AATCTCTGGA	GCCAGCTTCT	AGAGGTAGGA	AAGAGAAGAT	GTTCATTATC

7570	7580	7590	7600	7610	7620	7630	7640	7650
*	*	*	*	*	*	*	*	*
AGATAATGCA	AGAGAAGCAA	TTCGTCAGTT	TCACTGGGTA	TCTGCAAGGC	TTATTGATTA	TTCTAATCTA	ATAAGACAAG	TTTGTTGAAA

7660	7670	7680	7690	7700	7710	7720	7730	7740
*	*	*	*	*	*	*	*	*
TGCAAGATGA	ATACAAGCCT	TGGGTCCATG	TTTACTCTCT	TCTATTGGA	GAATAAGATG	GATGCTTATT	GAAGCCCAGA	CATTCTTGCA

7750	7760	7770	7780	7790	7800	7810	7820	7830
*	*	*	*	*	*	*	*	*
GCTTGGACTG	CATTTTAAGC	CCTGCAGGCT	TCTGCCATAT	CCATGAGAAG	ATTCTACACT	AGCGTCTGT	TGGGAATTAT	GCCCTGGAAT

7840	7850	7860	7870	7880	7890	7900	7910	7920
*	*	*	*	*	*	*	*	*
TCTGCCGTAA	TGACCTACG	CATCTCTCC	TCCTTGGACA	TTCCTTTGTC	TTCAATTGGT	GCTTTTGTT	TTCACCTCT	CCGTGATTGT

7930	7940	7950	7960	7970	7980	7990	8000	8010
*	*	*	*	*	*	*	*	*
AGCCCTACCA	GCATGTTATA	GGCAAGACC	TTTGTGCTTT	TGATCATTCT	GGCCCATGAA	AGCAACTTTG	GTCTCCTTTC	CCCTCTGTCT

8020	8030	8040	8050	8060	8070	8080	8090	8100
*	*	*	*	*	*	*	*	*
TTCCCGGTAT	CCCTTGGAGT	CTCACAAGGT	TTACTTTGGT	ATGGTTCTCA	GCACAAACCT	TTCAAGTATG	TTGTTTCTTT	GGAAAATGGA

8110	8120	8130	8140	8150	8160	8170	8180	8190
*	*	*	*	*	*	*	*	*
CATACTGTAT	TGTGTTCTCC	TGCATATATC	ATTCTCGAG	AGAGAAGGGG	AGAAGAATAC	TTTTCTTCAA	CAAATTTTGG	GGCCAGGAGA

8200	8210	8220	8230	8240	8250	8260	8270	8280
*	*	*	*	*	*	*	*	*
TCCCTTCAAG	AGGCTGCACC	TAAATTTTTC	TGTCTGTGT	GCAGGTCTTC	ATATAACTT	TACCAGGAAG	AAGGGTGTGA	GTTTGTGTT

FIG.17J



8290 8300 8310 8320 8330 8340 8350 8360 8370  
\* \* \* \* \*  
TTTCGTGTA TGGCCCTGGT CAGTGTAAG TTTTATCCTT GATAGTCTAG TTAATATGAC CCTCCCCACT TTTTAAAAAC CAGAAAAAGG  
8380 8390 8400 8410 8420 8430 8440 8450 8460  
\* \* \* \* \*  
TTTGAATGT TGAATGACC AAGAGACAAG TTAACGCTG CAAGAGCCAG TTACCCACCC ACAGGTCCCC CTACTTCCTG CCAAGCATTG  
8470 8480 8490 8500 8510 8520 8530 8540 8550  
\* \* \* \* \*  
CATTGACTGC CTGTATGGAA CACATTGTG CCAGATCTGA GCATTCTAGG CCTGTTTCAC TCACTCACCC AGCATATGAA ACTAGTCTTA  
8560 8570 8580 8590 8600 8610 8620 8630 8640  
\* \* \* \* \*  
ACTGTTGAGC CTTTCCTTTC ATATCCACAG AAGACACTGT CTCAAATGTT GTACCCCTGC CATTAGGAC TGAACCTTCC TTAGCCCAAG  
8650 8660 8670 8680 8690 8700 8710 8720 8730  
\* \* \* \* \*  
GGACCCAGTG ACAGTTGCTT TCCGTTTGTG AGATGATCAG TCTCTACTGA TTATCTTGCT GCITAAAGGC CTGCTACCA ATCTTTCTTT  
8740 8750 8760 8770 8780 8790 8800 8810 8820  
\* \* \* \* \*  
CACACCGTGT GGTCCGTGTT ACTGGTATAC CCAGTATGTT CTCACTGAAG ACATGGACTT TATATGTTCA AGTGCAGGAA TTGAAAAGTT  
8830 8840 8850 8860 8870 8880 8890 8900 8910  
\* \* \* \* \*  
GGACTTGTTT TCTATGATCC AAAACAGCCC TATAAGAAGG TTGGAAAAGG AGGAATAATA TAGCAGCCTT TGCTATTTTC TGCTACCATTT  
8920 8930 8940 8950 8960 8970 8980 8990 9000  
\* \* \* \* \*  
TCTTTTCCTC TGAAGCGGCC ATGACATTCC CTTGGCAAC TAACGTAGAA ACTCAACAGA ACATTTTCCT TTCCTAGAGT CACCTTTTAC  
9010 9020 9030 9040 9050 9060 9070 9080 9090  
\* \* \* \* \*  
ATGATAATGC ACAACTATAG ACTTGCTCAT TGTTGAGACT GATTGCCCTT CACCTGAATC CACTCTCTGT ATTCATGCTC TTGGCAATTT  
9100 9110 9120 9130 9140 9150 9160 9170 9180  
\* \* \* \* \*  
CTTTGACITT CTTTAAAGG CAGAAGCATT TTAGTTAATT GTAGATAAG AATAGTTTTT TTCCTCTTCT CCTTGGGCCA GTTAATAATT  
9190 9200 9210 9220 9230 9240 9250 9260 9270  
\* \* \* \* \*  
GGTCCATGCC TAACTGCAA CTCCGTCCA GTGCTGTGAT GCCATGACA CCTGCAAAAT AAGTTCTGCC TGGCATTTT GTAGATATTA

FIG.17K

9280	9290	9300	9310	9320	9330	9340	9350	9360
*	*	*	*	*	*	*	*	*
ACAGGTGAAT	TCCCGACTCT	TTTGGTTTGA	ATGACAGTTC	TCATTCCTTC	TATGGCTGCA	AGTATGCATC	ACTGCITCCC	ACTTACCTGA
9370	9380	9390	9400	9410	9420	9430	9440	9450
*	*	*	*	*	*	*	*	*
TTTGTCTGTC	GGTGGCCCCA	TATGGAAACC	CTGCGTGTCT	GTTGGCATAA	TAGTTTACAA	ATGGTTTTTT	CAGTCCTATC	CAAATTTATT
9460	9470	9480	9490	9500	9510	9520	9530	9540
*	*	*	*	*	*	*	*	*
GAACCAACAA	AAATAATTAC	TTCTGCCCTG	AGATAAGCAG	ATTAAGTTTG	TTCAATTCTCT	GCTTTATTCT	CTCCATGTGG	CAACATTCTG
9550	9560	9570	9580	9590	9600	9610	9620	9630
*	*	*	*	*	*	*	*	*
TCAGCCTCTT	TCATAGTGTG	CAAACATTTT	ATCATTCTAA	ATGGTCACTC	TCGCCCCTTG	GACCCATTTA	TTATTCACAG	ATGGGGAGAA
9640	9650	9660	9670	9680	9690	9700	9710	9720
*	*	*	*	*	*	*	*	*
CCTATCTGCA	TGGACCCTCA	CCATCCTCTG	TGCAGCACAC	ACAGTGCAGG	GACCCAGTGG	CGATGGCGAT	GACTTTCTTC	CCCTGGGAAT

TCC

FIG.17L

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